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Best Local
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mussel, Mytilus edulis.";
Eur. J. Biochem. 267:4970-4977(1999)
                                       Xu B., Hellman U., Ersson B., Janson J.-C.; "Purification, characterization and amino-acid sequence analysis thermostable, low molecular mass endo-beta-1,4-glucanase from blue thermostable in the first the first thermostable in the first the first thermostable in the first thermostable in the first the 
                                                                                                                      TISSUE-Digestive gland; meDLINE-20389517; PubMed-10931178;
                                                                                                                                                                                                                        Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia;
Mytiloidea; Mytilidae; Mytilus.
MCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                             16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Endoglucanase (EC 3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT_SITE
ACT_SITE
ACT_SITE
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                                                                                                                                                                         SEQUENCE, FUNCTION, AND MASS SPECTROMETRY
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                                                                                                                                                                                                                                                                                                                                     (CMCASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              P82186;
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PROSITE; PS00139; THIOL_PROTEASE_CYS; PROSITE; PS00639; THIOL_PROTEASE_HIS; PROSITE; PS00640; THIOL_PROTEASE_ASN.
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InterPro; IPR000169; Thiolprot_act_site.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SCFPYTAKDSP--CKPRENCLRYYSSDYYYVGGFYGGCNEALMKLELVKHGPMAVAFEVH 376
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462 AA;
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1.1;
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                                                                                                                                                                                                                                                                                    01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
01-APR-1990 (Rel. 41, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pollen allergen Lol p 2-A (Lol p II-A),
Lolium perenne (Perennial ryegrass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Poaceae; Pooldeac
                                                                                                                                                 Ansari A.A., Shenbagamurthi P., Marsh D.G.; "Complete amino acid sequence of a Lolium pgrass) pollen allergen, LoI p II.", J. Biol. Chem. 264:11181-11185(1989).

-I. SUBCELLULAR LOCATION: Secreted.
-I. SUBCELLULAR COLORION: Secreted.
              Allergen;
DOMAIN
                                                PIR; A34291; A34291.
HSSP; P43214; 1WHO.
InterPro; IPR000882; Pollen_allergen; 1.
Pfam; PF01357; Pollen_allergen; 1.
ProDom; PD002179; Pollen_allergen; 1.
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                                       ProDom; PD002179; Pollen_allergen; PROSITE; PS50843; EXPANSIN_CBD; 1.
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-!- MISCELLANEOUS: Has an isoelectric point of 7.6. Its optimum pH is
4.6 and optimum temperature is between 30-50 degress celsius.
-!- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
                                                                                                                                                                                                                                       MEDLINE=89291864; PubMed=2472390;
                                                                                                                                                                                                                                                       SEQUENCE
                                                                                                                                                                                                                                                                                 NCBI_TaxID=4522;
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PROSITE; PS01140; GLYCOSYL_HYDROL_F45;
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                                                                                                                          SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FUNCTION: ACTIVE TOWARDS THE SOLUBLE CARBOXYMETHYLCELLULOSE (CMC).
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CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
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Multigene family.
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29 29
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NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
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             EXPANSIN-LIKE CBD
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Pred. No. 0
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Matches 27
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VARIANT
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                                                                                                                                                                                                                                                                                                    PRELIMINARY SEQUENCE OF 1-938 FROM N.A.

MEDLLINE-84272624; Pubmed-6087316;
Carlson J., Fuchs J.A., Messing J.;
"Primary structure of the Escherichia coli ribonucleoside diphosphate reductase operon.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Yamamoto Y., Aiba H., Baba T., Hayashi K., Inada T., Isono K., Itoh T., Kimura S., Kitagawa M., MaKino K., Miki T., Mitsuhashi N., Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nashimoto H., Oshima T., Oyama S., Saito N., Sampel G., Satoh Y., Sivasundaram S. Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Blattner F.R., Plunkett G. III, Bloch C.A., Riley M., Collado-Vides J., Glasner J.D., Ro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed=9278503;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Construction of a contiguous 874-kb sequence of the Escherichia coli-
KI2 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features.";
DNA Res. 4:91-113(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gregor J., Davis N.W., Kirkpatrick H.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hypothetical protein yfaL precursor.
  "The
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YFAL OR B2233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                             Hussain K., Elliott
                                                       MEDLINE=88201664; PubMed=2834621;
                                                                                                       SEQUENCE OF 1180-1250 FROM N.A.
                                                                                                                                                                                                             STRAIN=K12
                                                                                                                                                                                                                                     SEQUENCE OF 925-1198 FROM N.A.
                                                                                                                                                                                                                                                                                    Proc. Natl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yamagata S., Horiuchi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                64
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ain K., Elliott E.J., Salmond parD-mutant of Escherichia co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complete genome sequence of sec 277:1453-1474(1997).
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                                                                                                                                                       (JUN-1995) to
                                                                                                                                                                               O'Keeffe T.,
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                                                                                                                                                                                                                                                                                    Acad. Sci. U.S.A. 81:4294-4297(1984).
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                                                                                                                                                       Robison K., Church G.M.
o the EMBL/GenBank/DDBJ
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       coli
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                               G.P.C.;
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No. 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rode C.K., Mayhew G.F.
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          carries
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     a gyrAam mutation
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; D90855; BAA16052.1; ALT_INIT EMBL; D90854; BAA16050.1; ALT_INIT EMBL; K02672; -; NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   three gene classes.";

Nucleic Acids Res. 23:3554-3562(1995).

-!- SIMILARITY: TO E.COLI YDEK.

-!- CAUTION: REF.3 SEQUENCE DIFFERS EX
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Borodovsky M., McIninch J., Koonin E.V., Rudd K.E., Medigue C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=96032851; PubMed=7567469;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The complete sequence of gyrA."; Mol. Microbiol. 1:259-273(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hypothetical protein; SIGNAL 1 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000313; AAC75293.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Detection of new genes in a bacterial genome using Markov models
                                                                                                                                                                                                                                                                                                                                                                    CONFLICT
                                                                                                                                                                                                                                                                                                                                                                               CONFLICT
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                        187 LRGQSLSFQVTDSDGRTVVSYDVV
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                                                                                                  NIDAGG------NVTVNQGSF-----AGII------EGAG-QLTIAQNGSYVL 452
                                                                                                                                                                                                         GKTLVIGNTENDGAVDSTAGTGLITKTGSGDLVLNADNNDFTGEMQIENGEVTLGRSNSL 364
NDG----LEVSGSSGTVIGSQDVV
                                                 AGAQSMALTGDIVVDDGAVLSLEGDAADLTALQDDPQSIVLNGGVLDLSDFSTWQSGTSY 512
                                                                                                                               ANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVPVAFRRVPCEKGGGIRFTINGNPYFDL 145
                                                                                                                                                         MNVG-----DTHCQDDPQDCYGLTIGSIDQYQNQAELNVGSTQQTFVHALTGFQNGTL 417
                                                                                                                                                                                  FNSGQKCGACFELTCEDDPEWCIP---GSIIVRYNLA-------
                                                                                                                                                                                                                                   GHATFYGGADASGTMGGACGYGNLHSQGYG------LQ-----TAALSTAL 47
                                                                           VLITNVGGAGDI-----RAVSLKGSKT-----DQWQSMSRNWG-----QNWQSNT-Y 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        U30459; AAA74094.1;
Y00544; -; NOT_ANNC
                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                 AA;
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1250
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Repeat;
                                                                                                                                                                                                                                                                24;
                                                                                                                                                                                                                                                                                                                                                                                                      K -> Q (IN REF. 3).
LV -> PG (IN REF. 3).
S -> Q (IN REF. 3).
                                                                                                                                                                                                                                                                            Score 85.5; DB 1; Pred. No. 6.4;
                                                                                                                                                                                                                                                                                                                            A -> R (IN REF. 3).
E -> S (IN REF. 3).
V -> M (IN REF. 3).
PP -> AT (IN REF. 3).
PAYQPVLNAKVGGYLNNLRAANQAFMMERRDHAGGDGQTLN
LRVIGG -> LLTSRC (IN REF. 4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYPOTHETICAL PROTEIN YFAL 15 x 2 AA TANDEM REPEATS (AAV -> RGRS (IN REF. 3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Signal;
                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                  17F98C05E299FC95 CRC64;
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3).
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                                                                                                                                                                                                                                                                                        Length 1250;
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                                                                                                                                                                                   ----NFAL 85
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CATC_HUMAN

RESULT 14

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EMBL; X87212; CAA60671.1; -. EMBL; U79415; AAC51341.1; -. HSSP; O46427; BPCH.
                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Toomes C., James J., Wood A.J., Wu C.L., McCormick D., Lench N., Hewitt C., Moynihan L., Roberts E., Woods C.G., Markham A., Wong Midmer R., Ghaffar K.A., Pemberton M., Hussein I.R., Temtamy S.A. Davies R., Read A.P., Sloan P., Dixon M.J., Thakker N.S., Loss of function mutations in the cathepsin C gene result in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  periodontal disease and palmoplantar keratosis.";
Nat. Genet. 23:421-424(1999).
-1- FUNCTION: THIOL PROTEASE. HAS DIPEPTIDYLPEPTIDASE ACTIVITY. CAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VARIANTS PLS F-249; L-252; P-272; S-301; MEDLINE-20047769; PubMed-10581027;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dipeptidyl-peptidase I precursor (EC 3.4.14.1) (DPP-I) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase).
CTSC OR CPPI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Paris A., Strukelj B., Pungercar J., Renko M., Dolenc I., Turk V.; "Molecular cloning and sequence analysis of human preprocathepsin C."; FEBS Lett. 369:326-330(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eurezo
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-95377428; PubMed-7649281;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human dipeptidyl-peptidase I. Gene characterization, localization,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WEDLINE=97248590; PubMed=9092576;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                              SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN CROSS-LINKED BY A DISULFIDE BOND.

SUBCELLULAR LOCATION: LYSOSOMAL.

DISEASE: DEFECTS IN CTSC ARE A CAUSE OF PAPILLON-LEFEVRE SYNDROME (PLS) ALSO KNOWN AS KERATOSIS PALMOPLANTARIS WITH PERIODONTOPATHIA. IT IS AN AUTOSOMAL RECESSIVE DISORDER THAT IS MAINLY ASCERTAINED BY DENTISTS BECAUSE OF THE SEVERE PERIODONTITIS THAT AFFLICTS PATIENTS. BOTH THE DECIDIOUS AND PERMANENT DENTITIONS ARE AFFECTED, RESULTING IN PREMATURE TOOTH LOSS. PALMOPLANTAR KERATOSIS, TYPICALLY DEVELOPS WITHIN THE FIRST THREE YEARS OF LIFE. KERATOSIS ALSO AFFECTS OTHER SITES SUCH AS ELBOWS AND PERMANENT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Biol.
                                           OPS; C01.070; -.
; 602365; -.
; 245000; -.
                                                                                                                                                                                                                     European Bioinformatics Institute. The by non-profit institutions as long
                                                                                                                                                                                                                                                                                               AND KNEES.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS PAPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Xbb-|-
KCC, except when Xaa is Arg or Lys, or Xbb or Xcc is Pro.
COFACTOR: REQUIRES CHLORIDE IONS FOR ACTIVITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       expression.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DEGRADE GLUCAGON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chem. 272:10260-10265(1997).
IPR000668; Peptidase_C1.
IPR000169; Thiolprot_act_site
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rao G.V., Hoidal J.R.;
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                                                                                                                                                                                                               There are no restrictions on ong as its content is in no
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                                                                                                                                                                                                                                                       GUN2_TRIRE
                                                                                                                                                                                                                                                                  RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
Gene
[2]
             Saloheimo M., Lehtovaara P., Penttilae M., Teeri T.T., Staahlberg Johansson G., Pettersson G., Clayssens M., Tomme P., Knowles J.K.C. "EGIII, a new endoglucanase from Trichoderma reesel: the characterization of both gene and enzyme.";
                                                                                                                 Trichoderma reesei (Hypocrea jecorina).
Eukaryota, Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreales; Hypocreaceae; Hypocrea.
                                                               STRAIN=VTT-D-80133;
MEDLINE=88255850; PubMed=3384334;
                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                Endoglucanase
                                                                                                                                                                                           01-AUG-1988
15-JUL-1999
                                                                                                                                                                                                                               GUN2_TRIRE P07982;
                                                                                                                                                           EGL2 OR EGLII.
                                                                                                                                                                        (Cellulase)
                                                                                                                                                                                                                  01-AUG-1988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00112; Peptidase_C1; 1.
PRINTS; PR007705; PAPAIN.
PROSITE; PS000139; THIOL_PROTEASE_CYS;
PROSITE; PS00639; THIOL_PROTEASE_HIS;
PROSITE; PS00640; THIOL_PROTEASE_ASN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VARIANT
                                                                                                                                                                                                                                                                                                                                                             112 ---- OYRAGIVPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKT 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ACT
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                                                                                                                                                                                                                                                                                                                                                                                                        56 ACFELTCEDDPEWCIPGSIIVRYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIA---- 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
         63:11-21(1988).
                                                                                                                                                                                                                                                                                                                                                                                  ACFPYTGTDSP--CKMKEDCFRYYSSEYHYVGGFYGGCNEALMKLELVHHGPMAVAFEVY 377
                                                                                                                                                                                                                                                                                                DSASGMDYWIVKNSWGTGWGENGYFR 440
                                                                                                                                                                                                                                                                                                                     DQWQSM-----SRNWGQNWQSNTYLR 188
                                                                                                                                                                                                                                                                                                                                        DDFLHYKKGIYHHTGLRDPF-----NPF----ELTN-----HAVLLVGYGT
                                                                                                                                                                                                                                                                                                                                                                                                                                      l Similarity
37; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 463 AA;
                                                                                                                                                                                         (Rel. 08, Last sequence update) (Rel. 38, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Thiol protease; Lysosome; Glycoprotein; Zymogen; Signal;
                                                                                                                                                                                                                (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              339
                                                                                                                                                                         kel. 38, Last annotation update)
EG-II precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase)
                                                                                                                                                                                                                                        STANDARD;
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/FTId=VAR_009542.

R -> P (IN PLS).

/FTId=VAR_009543.

G -> S (IN PLS).
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Pred. No.
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Y -> C (I
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BY SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             759B5EF1290C3771 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                   62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 463,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN)
                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claeyssens M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=93131031;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ACTIVE SITE GLU-350.
                                                                                                                                                                                                                                                                                                                         DISULFID
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS00562; CBD_FUNGAL; 1.
PROSITE; PS00659; GLYCOSYL_HYDROL_F5; 1.
Cellulose degradation; Hydrolase; Glycosidase; Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00734; CBD_1; 1.
Pfam; PF00150; cellulase; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S28372; S28372.
HSSP; P00725; 2CBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD001821; CBD_SMART; SM00236; fCBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000254; CBD_fungal
InterPro; IPR001547; Glyco_hydro_F5.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M19373; AAA34213.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SIGNAL
                                                                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                    DISULFID
                                                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                 MOD_RES
                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
168 LDSTSISKYDQLVQGCLSLGAYCIVDIHNYARWNGGIIGQGGPTNAQFTSLWSQLASKYA 227
                            134 RETINGNPYEDLVL--------ITNVGGAGDIRAVSLKGSKTDQWQ 171
                                                           115 TSKVYPPLKNFTGSN-----NYPDGIGQMQHFVNEDGMTIFRLPVGWQYLVNNNLGGN 167
                                                                                                                                                                                                               13 YGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKC---GACFELTCEDDPEW- 68
                                                                                           94
                                                                                                                                                        69
                                                                                                                                                                                  16 YGGAVAQQTVWGQCG-----GIG-----WSGPTNCAPGSACSTL----NPYYA 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE
GENERALLY REQUIRES THREE TYPES OF HYDROLYTIC ENZYMES:

(1) ENDOGLUCANASES WHICH CUT INTERNAL BETA-1, 4-GLUCOSIDIC BONDS;

(2) EXOCELLOBIOHYDROLASES THAT CUT THE DISSACCHARIDE CELLOBIOSE
FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
FROM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;

(3) BETA-1, 4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE AND OTHER
SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAUTION: WAS ORIGINALLY CALLED ENDOGLUCANASE EG-III.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SIMILARITY: BELONGS TO CELLULASE FAMILY A (FAMILY 5 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic linkages in cellulose.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYDROLASES).
SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
                                                                                                                      QCIPGATTITTSTRPPSGPTTTTRATSTSSSTPPTSSGVRFAGVNIAGEDFGCTTDGTCV 114
                                                                                           ----NPPLKHFDLAEPAFLQIAQYRAGI------
                                                                                                                                                        -CIPGSII-----
                                                                                                                                                                                                                                                64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          van Beeumen J., Henrissat B., de la Mata I.,
                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                         122
22
22
22
22
22
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239
350
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CBD_fungal; 1.
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418
57
91
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                                                                                                                                                                                                                                                               6.5%;
                                                                                                                                                                                                                                                                                                             44227 MW;
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                                                                                                                                                                                                                                                                  Score 81;
Pred. No.
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BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                            NUCLEOPHILE
                                                                                                                                                                                                                                                                                                                                    PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                   LINKER
                                                                                                                                                                                                                                                                                                                                                                                                                                                 CELLULOSE-BINDING (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                ENDOGLUCANASE EG-II.
                                                                                                                                                                                                                                                                                                             26A492D55237A49B CRC64;
                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                          -----VRY---NLANFALANDNGGWC- 93
                                                                                                                                                                                                                                                                               DB 1; Length 418;
                                                                                                -----VPVAFRRVPCEKGGGI 133
                                                                                                                                                                                                                                                    77;
                                                                                                                                                                                                                                                     Indels 152;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         restrictions on
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Search completed: October 11, 2002, 14:57:33 Job time : 6.81181 secs

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Result
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Maximum DB seq length: 2000000000
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Perfect score:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1203.5
        Score
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Match
       BLOSUM62
Gapop 10.0 , Gapext 0.5
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1245
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probable expansin
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                homolog
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RESULT 2 T10079 T10079 expansin S1 precursor - cucumber C;Species: Cucumis sativus (cucumber) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-200 C;Accession: T10079 R;Shcherban, T-Y; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995	RESULT 1 T50656 expansin EXP2 [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 21-ul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul C:Accession: T50566 R:Shoherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-P Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995 A;Title: Molecular cloning and sequence analysis of expansinsa highl A;Accession: T50656 A;Status: preliminary; translated from GB/EMBL/DDBJ A;Rolecule type: mRNA A;Residues: 1-255 <shc> A;Roseription: induces extension (creep) in plant cell walls C;Genetics: C;Genetics: A;Gene: EXP2 C;Function: A;Bescription: induces extension (creep) in plant cell walls C;Keywords: cell wall Ouery Match Best Local Similarity 96.5%; Pred No. 9;1e-102; Matches 220; Conservative 1; Mismatches 4; Indels 3; (; DB 2; Length 725; Best Local Similarity 96.5%; Pred No. 9;1e-102; Matches 220; Conservative 1; Mismatches 4; Indels 3; (; DB 2 LongGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLOTAALSTALFNSGOKCGACFEL Db 28 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLOTAALSTALFNSGOKCGACFEL Oy 1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLOTALSTALFNSGOKCGACFEL OY 1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLOTAALSTALFNSGOKCGACFEL OY 1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLOTAALSTALFNSGOKCGACFEL OY 1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLOTAALSTALFNSGOKCGACFEL OY 1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLOTAALSTALFNSGO</shc></shc></shc></shc></shc>	ALIGNMENTS	30 758.5 60.9 261 2 T03737 31 694.5 55.8 255 2 T03299 32 619 49.7 160 2 T09871 33 609 48.9 257 2 G96654 34 602 48.4 257 2 F866259 35 532 42.7 256 2 T05648 36 287 23.1 77 2 T09815 37 278.5 22.4 262 2 T09828 38 272 21.8 102 2 T09828 39 272 21.8 102 2 T09828 40 266.5 21.4 491 2 F96681 41 266 21.4 261 21.0 277 2 \$48032 43 259 20.8 257 2 \$48032 44 259 20.8 271 2 H84592 45 257 20.6 263 2 \$13614
Jul-2000 m-Mason, S.J	Me-Jul-2000 Gen-Mason, S.J.; highly conserved highly conserved 1; 1; 1; 1; 3; Gaps 1; 3; Gaps 1; ACFEL 87 ACFEL 87 AFRAGI 117 1111 4SRNW 177 4SRNW 207		n - rice la - ri
shi.	red, mu		

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A; Molecule type: mRNA
A; Residues: 1-250 <SHC>
A; Cross-references: EMBL: U30382; NID: 91040874; PIDN: AAB37746.1; PID: 91040875
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Reference number: Z14894; MUID:96016146
A;Accession: T10079
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Superfamily: expansin 
F;1-23/Domain: signal sequence #status predicted <SIG>
F;24-250/Product: expansin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: cultivar Burpee Pickler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Description: mediates cell wall extension
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable expansin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: F84831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benlo, M.I.; IOWI, C.D.; Fuji, C.M.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: F84831
R; Lin, X.; Kaul, S.
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C; Superfamily:
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C;Genetics:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                       ;Superfamily: expansin
                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              144 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTG-WQSMSRNW 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      178 GQNWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  24
                            116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFEL 60
                                                                                                          61 TCEDDPEWCIPGSIIVRYNLANF-----ALANDNGGWCNPPLKHFDLAEPAFLQIAQYRA 115
                                                                                                                                                  26 DDGGWQGGHATFYGGEDASGTMGGACGYGNLYGQGYGTNTAALSTALFNNGLTCGACYEM 85
                                                                                                                                                                                          1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFEL 60
                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGI 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCEDDPEWCIPGSIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGI 117
                          GIVPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSR 175
                                                                    KCNDDPRWCLGSTITV--TATNFCPPNPGLSNDNGGWCNPPLQHFDLAEPAFLQIAQYRA 143
171;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           l Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                           GB:AE002093; NID:g2651297; PIDN:AAB87577.1; GSPDB:GN00139
                                                                                                                                                                                                                                                               77.0%;
74.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26; Mismatches
                                                                                                                                                                                                                                             23; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 962; DB 2;
Pred. No. 7.4e-80;
                                                                                                                                                                                                                                           Score 958.5; DB 2;
Pred. No. 1.6e-79;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2; Length 250;
                                                                                                                                                                                                                                                                                     DB 2; Length 253;
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                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Reference number: Z16866
A; Accession: T09821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Residues: 1-232 <HUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Status: preliminary; translated from GB/EMBL/DDBJ
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A; Accession: T09826
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                    QУ
                                                                당
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                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-232 <HUT>
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                                                                                                                                                                                        Query Match
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                        63
                                                                                                                                                                        Local
                                                                œ
                    EDDPEWCIPGSIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVP 119
                                                              GGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMQC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              164;
                                                                                                                                                    164;
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                                                                                                                                                                      Similarity
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                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.5%; Score 927; DB 2
72.9%; Pred. No. 1e-76;
                                                                                                                                                                        74.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26; Mismatches
                                                                                                                                                       26;
                                                                                                                                                                           Pred. No. 1e-76;
                                                                                                                                                       Mismatches
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R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library, July 1996
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C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         expansin (clone pPtexp5) - loblolly pine (fragment)
C;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U64891; NID:g1778100; PID:g1778101
                                                                                                                                                                                                                                A;Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105
A;Experimental source: clone pPtexp5
                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, July 1996
A;Description: Expansing are conserved in conifers and expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 GIVPVSFRRVPCMKKGGIRFTINGHSYFNLVLISNVGGAGDVHAVSIKGSKTQSWQAMSR 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              176 NWGQNWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               180 NWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                120 VAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           187 NWQSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSNWQFGQTFEGSQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68 NDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIVP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELTC 62
3 GGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELFC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EDDPEWCIPGSIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMRC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
                                                                                                                                                     Score 927; DB 2; Length 232;
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                                                                                                       31;
                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 in response to exoge
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                                                                                                       Gaps
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A:Cross-references: EMBL:U64892; NID:g1778102; PID:g1778103
A:Experimental source: clone pPtexp4
C:Superfamily: expansin
                                                                                                                                                                                                                                      R:Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library, July 1996
N:Description: Expansing are conserved in conifers and expressed in
                                                                                                                                                                                                                                                                           expansin (clone pPtexp4) - loblolly pine (fragment)
c;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change
C;Accession: T09825
R;Hutchison, K,W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
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T09818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Accession: T09818
R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library, July 1996
A;Description: Expansins are conserved in conifers and expressed A;Reference number: Z16866
A;Accession: T09818
                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-232 <HUT>
                                                                                                                                                                                                     A; Reference number: Z16866
A; Accession: T09825
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C;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                           T09825
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A; Residues: 1-232 <HUT>
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                   Local Similarity 71.0 nes 161; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68 NDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKTAKYRGGIVP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63
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Local Similarity 72.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                             NWOSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQ 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQ 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   163;
                                                                                          expansin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         73.3%; Score 912; DB 2; 71.6%; Pred. No. 2.3e-75;
                   27;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 923; DB 2; Pred. No. 2.3e-76;
                   Mismatches
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                                                                               expansin - rice
c;Specles: Oryza sativa (rice)
C;Date: 23-Apr:1999 #sequence_revision 23-Apr:1999 #text_change
C;Accession: T04175
R;Cho, H.T.; Kende, H.
Plant Cell 9, 1661-1671, 1997
                                A; Title: Expression of expansin genes is correlated with A; Reference number: 215042; MUID:97480100 A; Accession: T04175
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           A; Status: preliminary; translated from GB/EMBL/DDBJ
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T09786
A; Molecule
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C; Superfamily:
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C; Genetics:
A; Gene: GhEX1
C; Function:
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Biophin. Biophys. Acta 1398, 342-6, 1998
A;Title: Specific expression of an expansin gene
A;Reference number: Z14468; MUID:9655931
A;Accession: T09786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expansin - upland cotton
c;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C;Accession: T09786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-258 <ORF>
A; Cross-references: EMB
                                                                                                                                                                                                                                                                                                                                                                                       A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Status: preliminary; translated from GB/EMBL/DDBJ
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             GONWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
                                                                                                                                                            TCEDDPEWCIPGSIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGI 117
GQNWQSNAYLNGQSLSFKVTASDGRTITAYNVVPAGWQFGQTFEGGQF
                                                                                         VPVAFRRVPCEKGGGIRETINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW 177
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                                                                    VPVMFRRVSCVKKGGIRYTMNGHSYFNMVLITKLGGAGDITSVSIKGSRTG-WLPMSRNW
                                                                                                                                           RCNNDPQWCISRTITVTATNFCPPNYALSSDNGGWCNPPREHFDLAEPRFLRIAEYRAGI
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se: cultivar Siokra 1-2
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                                                                                                                                                                                                                                                                                       Score 912; DB 2; LC
Pred. No. 2.6e-75;
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26-May-2000

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C; Function:
A; Description:
C; Superfamily:
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A;Cross-references: EMBL:U85246; NID:g1815680; PIDN:AAB81662.1; PID:g1815681
A;Experimental source: cv. Pin Gaew 56
C;Genetics:
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R;Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Shieh, R;Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Shieh, Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A;Title: Molecular cloning and sequence analysis of expansins—a highly conserved, multi-A;Reference number: Z14894; MUID:96016146
A;Accession: T03298
                       RESULT 11
T50654
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C;Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expansin 2 - rice
C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
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                                                                                                                                                                                                                                  VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWQSNAFLDGQSLSFQVTASDGRTVTSNNVAHPGWQFGQTFEGGQF 246
                                                                                                                  GQNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFXQTFEGGQF 251
                                                                                                                                                          GQNWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
                                                                                                                                                                                                                                                                                                  RCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGI 144
                                                                                                                                                                                                                                                                                                                                             TCEDDPEWCIPGSI-IVRYNLA--NFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGI 117
                                                                                                                                                                                                                                                                                                                                                                                           DYGSWQSAHATFYGGGDASGTMGGACGYGNLYSTGYGTNTAALSTVLFNDGAACRSCYEL 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     160;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 induces extension (creep) in plant cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.0%;
71.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        70.9%; Score 883; DB 2; 70.2%; Pred. No. 1.1e-72;
  Arabidopsis thaliana (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 884; DB 2;
Pred. No. 8.7e-73;
3; Mismatches 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 2; Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 2; Length 251;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                               203
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R;Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Shi proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A;Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description: induce C; Superfamily: expans C; Keywords: cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QУ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:U30476; C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Reference number: Z14894; MUID:96016146 A; Accession: T50654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession: T50654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Qy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: EXP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Residues: 1-237 <SHC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: preliminary; translated from GB/EMBL/DDBJ
당
                                          QУ
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                                                                                                                                      γ
                                                                                                                                                                                                                                                                                   C; Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-248 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: A84420; MUID: 20083487
A; Accession: C84444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 probable expansin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C84444
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                                                                                                                                                                                                                                                                                                            A; Map position:
                                                                                                                                                                                                                                                                                                                                     A; Gene: At2g03090
                                                                                                                                                                                                                                                                                                                                                            C; Genetics
                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: C84444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    180 NWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQ 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 VAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          72 QNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVP 131
  82
                                            62 CEDDPEWCIPGSIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIV 118
                                                                                         22 DAGWVNAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIK 81
                                                                                                                                                                                                                Toca T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GGWERCHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                       VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTG-WQAMSRNWGQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EDDPEWCIPGSIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVP 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC 71
  CQSDGAWCLPGAIIVTATNFCPPNNALPNNAGGWCNPPLHHFDLSQPVFQRIAQYKAGVV 141
                                                                                                                                                                                                                   Similarity
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                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                  GB:AE002093; NID:g3461833; PIDN:AAC32927.1; GSPDB:GN00139
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                                                                                                                                                                                                                69.7%; Score 868; DB 2; Length 248; 67.8%; Pred. No. 2.5e-71;
                                                                                                                                                                                            31;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (creep) in plant cell walls
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8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 869; DB 2
Pred. No. 1.9e-7
                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                               38; Indels
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A:Cross-references: EMBL:AC004684; NID:g3236234; PID:g3236246
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
                                                                                                                                                                                                                       R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thallana chromosome II BAC F13M22 genomic sequence.
A;Reference number: 214677
                                                                                                                                                                                                                                                                                                                  probable expansin F13M22.14 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress) c;Date: 05-Mar-1999 #sequence_revision 05-Mar-1999 #text_change 16-Feb-2001 C;Accession: T02530; C84795
                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-262 <ROU>
                                                                                                                                                                                      A; Status: translated from GB/EMBL/DDBJ
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C:Superfamily: expansin
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A;Accession: D84820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Lin, X.; Kaul, S.; Rouns
M.; Koo, H.; Moffat, K.S.;
euss, D.; Nierman, W.C.; V
Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         probable expansin [imported] - Arabidopsis thaliana (Spectes: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Feb.2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
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A; Residues: 1-257 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cross-references: GB:AE002093; NID:g2795809; PIDN:AAB97125.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             178 GQNWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            149 VPVSYRRVPCRKRGGIRFTINGHRYFNLVLITNVAGAGDIVRASVKGSRTG-WMSLSRNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 208 GQNWQSNAVLVGQALSFRVTGSDRRTSTSWNMVPSNWQFGQTFVGKNF 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       118 VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            89 ANDPOWCHSGSPSILITATNFCPPNLAQPSDNGGWCNPPREHFDLAMPVFLKIAQYRAGI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     63 EDDPEWCIPGSIIVRYNLANF-----ALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29 GAWQNAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGMSCGACFELKC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 QNWQSNNLLNGQALSFKVTASDGRTVVSNNIAPASWSFGQTFTGRQF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              179 QNWQSNTYLRGQSLSFQYTDSDGRTVYSYDVVPHDWQFGQTFEGGQF 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            68.4%; Score 851; DB 2 68.4%; Pred. No. 9e-70;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2; Length 257;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                43; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Introns: 52/1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Accession: T47689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Status: preliminary
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C; Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Experimental source: cultivar Columbia; BAC clone T22E16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A:Molecule type: DNA
A:Residues: 1-260 <BEN>
A:Cross-references: EMBL:AL132975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N;Alternate names: protein T22E16.160
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   expansin-like protein - Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Reference number: 224472
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Superfamily: expansin
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A:Accession: C84795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Introns: 54/1; 160/2
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                                          178 GQNWQSNTYLRGQSLSFQYTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
                                                                                                                                      92 VNDPKWCHPGNPSVFVTATNFCPPNLAQPSDNGGWCNPPRSHFDLAMPVFLKIAEYRAGT 151
                                                                                                                                                                              63 EDDPEWCIPGSITYRYNLANF-----ALANDNGGWCNPPLKHEDLAEPAFLQIAQYRAGI 117
                                                                                                                                                                                                                             213 GQNWQSNAVLIGQSLSFRVTASDRRSSTSWNVAPATWQFGQTFSGKNF 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 GONWOSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        154 VPVSYRRVPCRKIGGIRFTVNGFRYFNLVLVTNVAGAGDINGVSVKGSKTD-WVRMSRNW 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     118 VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW 177
                                                                                                                                                                                                                                                                          3 GGWERGHATFYGGADASGTWGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94 TDDPRWCVPGNPSILVTATNFCPPNFAQPSDDGGWCNPPREHFDLAMPMFLKIGLYRAGI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63 EDDPEWCIPG--SIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGI 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 GPWQNAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGFSCGACFEIKC
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                                                                                                                                                                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                                                                                                                                                                     68.0%; Score 846; DB 2; 67.5%; Pred. No. 2.6e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence Database, February 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   68.3%; Score 850; DB 2; Length 262; 68.9%; Pred. No. 1.1e-69;
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Db 211 GQNWQSNAVLVGQSLSFRVTSSDRRTSTSWNIAPSNWQFGQTFVGKNE 258

Search completed: October 11, 2002, 15:01:00 Job time : 11.2915 secs

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Result
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1: /cgn2_6/ptodata/2,

2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

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5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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US-08-440-517A-3
US-09-092-160-3
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US-09-362-642-2
US-08-440-517A-4
US-08-445-539-4
US-09-362-642-4
US-08-445-539-4
US-08-445-539-2
US-08-445-539-4
US-08-175-096-2
US-08-413-509-2
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(without alignments)
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| st I<br>tche<br>tche                                                                                                            | NOR-44 NO | 28<br>29<br>30<br>31<br>32<br>33<br>33<br>33<br>33<br>33<br>44<br>41<br>42<br>43<br>43<br>44<br>43<br>45                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| Call Simil 225; ( DNGGWERR                                                                                                      | D - PRESENTATION - 51                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 236.5 19 204 16 203 16 203 16 152 12 152 12 142 11 140 11 140 11 179.5 10 179.5 8 85.5 6 85.5 6 85.5 6 83 6                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   |
| ity serv TFYC TFYC TFYC TFYC TFYC                                                                                               | STEM: SEC 1  ORDER  ORD | 04 W G G G G G G G G G G G G G G G G G G                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |
| TOC<br>100<br>3ADAS<br>11111<br>11111<br>11111<br>11111<br>11111                                                                | on US/O  DANAAN, MA  ANN, TA  N PURI SES 6  ESS 6  ESS 6  EXIVANI NOLOGY PARK NIA STATES  ORN: DATA: STATES  ORN: DOS  REFECT I DATA: DOS  REFECT I DAT | 24<br>200<br>200<br>197<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145<br>145                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 |
| %;<br>0;<br>0;<br>HIII                                                                                                          | \ 74# H 7 C                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 200 S 20                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |
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| 243; UB 2; 0, 3.6e-128 tches 0; SQGYGLQTAAL             SQGYGLQTAAL             SQGYGLQTAAL CNPPLKHFDLA CNPPLKHFDLA CNPPLKHFDLA | IN PROTEINS OFFICE, THE VERSITY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | 08-441-507-24 08-431-507-5 08-431-974-4 08-433-288-4 08-433-288-4 08-441-507-2 08-441-507-1 08-441-507-2 08-441-507-2 08-441-507-3 08-441-507-3 08-441-507-3 08-441-507-8 08-441-507-8 08-441-507-8 08-441-507-8 08-441-507-8 08-441-507-8 08-144-121-2 08-426-428-2 08-426-428-2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             |
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| QKCGAC<br>             <br>           <br>                                                                                      | ນ<br>ນ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence<br>sequence                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| Caps<br>L 60<br>L 60<br>L 60<br>V 12<br>V 12                                                                                    | -                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | e 2, Apple |
|                                                                                                                                 |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | \\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        |

Вb

121 AFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQN 180

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GENERAL INFORMATION:

APPLICANT: COSGTOW, Daniel J

APPLICANT: GOUGEN-MASON, Simon

APPLICANT: Guiltinan, Mark J

APPLICANT: Shcherban, Tatyana

APPLICANT: Shcherban, Tatyana

APPLICANT: Shi, Jun

FITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS

FILE REFERENCE: 1194/IC114US3

CURRENT APPLICATION UNMBER: US/09/092,160C

CURRENT FILING DATE: 1998-06-05
 ; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis; OTHER INFORMATION: expansin US-09-092-160-5
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 US-09-092-160-5
 RESULT 3
US-09-092-160-7
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 SEQ ID NO 5
LENGTH: 225
 GENERAL INFORMATION:
 Sequence 5, Application US/09092160C Patent No. 6255466
 Sequence 7, Application US/09092160C Patent No. 6255466
 Matches
 Query Match
 EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DAYE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
 APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
 SOFTWARE: PatentIn Ver. 2.1
 FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARL@ER APPLICATION NUMBER: 08/440,517
 FEATURE:
 ORGANISM: Artificial Sequence
 TYPE: PRT
 181 WQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
 181
 121 AFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQN 180
 61 TCEDDPEWCIPGSIIVRYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVPV 120
 61 TCEDDPEWCIPGSIIVRYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVPV 120
 Local
 1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFEL 60
 1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFEL 60
 WQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
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 225;
 Similarity
 Conservative
 100.0%; Score 1245; DB 4; 100.0%; Pred. No. 3.6e-128;
 0;
 Mismatches
 Length 225;
 Indels
 0; Gaps
 0,:
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 US-09-092-160-7
 US-08-440-517A-6
 US-08-440-517A-6
 SEQ ID NO 7
LENGTH: 227
 Patent No. 5959082
 Query Match
Query Match
 Sequence 6,
 Matches
 EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
 GENERAL INFORMATION:
 SOFTWARE: PatentIn Ver. 2.1
 CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
 OTHER INFORMATION: Description of Artificial Sequence: cucumber OTHER INFORMATION: expansin
 FEATURE:
 ORGANISM: Artificial Sequence
 TYPE: PRT
 OPERATING SYSTEM: DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE,
ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
 COMPUTER READABLE FORM:
 APPLICANT: COSGROVE, DANIEL J.; APPLICANT: GUILTINAN, MARK;
 SEQUENCE CHARACTERISTICS:
 TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 APPLICANT:
 180
 118 VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW 177
 STREET: 113 TECHNOLOGY
CITY: UNIVERSITY PARK
 COMPUTER:
 61
 TOPOLOGY:
 TYPE:
 LENGTH:
 FILING DATE:
 APPLICATION NUMBER:
 MEDIUM TYPE:
 COUNTRY:
 61 TCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHEDMAEPAFLQIAQYRAGI 120
 1 DNGGWERGHATEYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSQQKCGACFEL 60
 Local Similarity
 1 DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 60
 GONWOSNNYLNGOGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
 GQNWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTG-WQSMSRNW 179
 TCEDDPEWCIPGSIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGI 117
 16802-7000
 AMINO ACID
 Application US/08440517A
 PENNSYLVANIA
 GUILTINAN, MARK;
SHCHERBAN, TATYANA;
 UNITED STATES OF AMERICA
 Conservative
 NEC 286
 UNKNOWN
 FLOPPY DISK
 JUN
 77.3%; Score 962; DB 4 75.0%; Pred. No. 3e-97;
 69.4%;
 US/08/440,517A
 26;
 Score 863.5;
 Mismatches
 DB 4; Length 227;
 DВ
 27; Indels
 2
 Length 226;
 4
 Gaps
 2
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Best Local Similarity

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 APPLICANT: COSTICUE, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Guiltinan, Mark J
APPLICANT: Schierban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/IC114US3
CURRENT APPLICATION NUMBER: US/99/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER APPLICATION NUMBER: 08/260,944
EARLIER FILING DATE: 1993-05-12
SCOTTANE: Patentin Ver. 2.1
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RESULT 6
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 Matches
 Query Match
 SEQ ID NO 6
 Sequence 6, Application US/09092160C
Patent No. 6255466
 GENERAL INFORMATION:
 Matches 158; Conservative
 TYPE: PRT
ORGANISM: Artlficial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis OTHER INFORMATION: expansin
 FEATURE:
 LENGTH: 226
 179 GONWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
 178 GONWOSNTYLRGOSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
 120 VPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTG-WQPMSRNW 178
 118 VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW 177
 61 TCEDDPEWCIPGSI-IVRYNLA--NFALANDNGGWCNPPLKHEDLAEDAFLQIAQYRAGI 117
 179 GONWOSNSYLDGOSLSFOVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
 120 VPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTG-WQPMSRNW 178
 118 VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW 177
 60 RCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGI 119
 178 GONWOSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
 1 DYSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 59
 1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFEL 60
 61 TCEDDPEWCIPGSI-IVRYNLA--NFALANDNGGWCNPPLKHEDLAEPAFLQIAQYRAGI 117
 Loca I
 60
 1 DNGGWERGHATFYGGADASGTWGGACGYGNLHSOGYGLOTAALSTALFNSGOKCGACFEL 60
 RCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGI 119
 DYSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 59
 158;
 Similarity
 Conservative
 69.4%; Score 863.5; DB 4; Length 226; 69.3%; Pred. No. 1.7e-86;
 69.3%; Pred No. 1 7e-86;
 24; Mismatches
 24; Mismatches 41;
 41;
 Indels
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 US-09-092-160-2
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 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simc
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
 US-08-440-517A-2
 US-08-440-517A-2
 Sequence 2, Application US/09092160C Patent No. 6255466
 APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/10114US3
 Matches
 Query Match
CURRENT APPLICATION NUMBER: US/09/092,160C CURRENT FILING DATE: 1998-06-05 EARLIER APPLICATION NUMBER: 08/440,517 EARLIER FILING DATE: 1995-05-12 EARLIER APPLICATION NUMBER: 08/242,090 EARLIER FILING DATE: 1994-05-12
 Sequence 2, Application US/08440517A Patent No. 5959082
 CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
 GENERAL INFORMATION:
 SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
 SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
 182
 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
 APPLICANT: COSGROVE, DANIEL J.
APPLICANT: GUILTINAN, MARK;
APPLICANT: SHCHERBAN, TATYANA;
APPLICANT: SHI, JUN
 180 NWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEG 222
 TITLE OF INVENTION:
 123 VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTG-WQAMSRNWGQ
 120 VAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDOWOSMSRNWGO 179
 63 QNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVP 122
 / Match 69.0%; Score 859; DB 2; Local Similarity 69.1%; Pred. No. 5.3e-86; Local Similarity 28: Mismatches 37;
 TOPOLOGY:
 TYPE: AMINO ACID
 STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
 FILING DATE:
 OPERATING SYSTEM:
 ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
 3 GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC 62
 APPLICATION NUMBER:
 3 GGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELTC 62
 LENGTH:
 NWQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTG 224
 16802-7000
 UNKNOWN
 UNITED STATES OF AMERICA
 SHI, JUN
 COSGROVE, DANIEL J.;
 NEC 286
 FLOPPY DISK
 PURIFIED EXPANSIN PROTEINS
 US/08/440,517A
 Simon
 DB 2; Length 228;
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 US-08-440-517A-3
 US-08-440-517A-3
 SEQ ID NO 2
LENGTH: 228
 Query Match
 Sequence 3, Application US/08440517A Patent No. 5959082
 EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
Query...Match
 GENERAL INFORMATION:
 OTHER INFORMATION: Xaa is unknown or other
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: rice expansin
 FEATURE:
 ORGANISM: Artificial Sequence
 TYPE: PRT
 NAME/KEY: UNSURE LOCATION: 211
 CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 APPLICANT:
APPLICANT:
APPLICANT:
 APPLICANT: SHCHERBAN, TATYANA;
APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
 COMPUTER READABLE FORM:
 CORRESPONDENCE ADDRESS:
 CURRENT APPLICATION DATA:
 182
 180 NWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEG 222
 120 VAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQ 179
 63 QNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVP 122
 63
 ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY STREET: 113 TECHNOLOGY CENTER
 Local Similarity
 3 GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC 62
 3 GGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELTC 62
 TYPE: AMINO ACID
 COMPUTER:
 COUNTRY:
 CITY: UNIVERSITY PARK
 FILING DATE
 APPLICATION NUMBER: US/08/440,517A
 SOFTWARE:
 OPERATING SYSTEM:
 MEDIUM TYPE:
 TOPOLOGY:
 LENGTH:
 EDDPEWCIPGSIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVP 119
 154;
 16802-7000
 PENNSYLVANIA
 COSGROVE, DANIEL J.;
GUILTINAN, MARK;
 Conservative
 UNITED STATES OF AMERICA
 WORDPERFECT 5.1
 NEC 286
 UNKNOWN
 FLOPPY DISK
 69.0%;
69.1%;
 DOS
 62.4%;
 28; Mismatches
 Score 859; DB 4;
Pred. No. 5.3e-86;
 Score 777.5;
 DB 4; Length 228;
 DB 2;
 37;
 Indels
 Length 222;
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 Gaps
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 SEQ ID NO 3
 GENERAL INFORMATION:
 Best Local Similarity 64.18;
 Sequence 3, Application US/09092160C Patent No. 6255466
 Matches
 Matches 143;
 Query Match
 APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
 EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
 APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
 CURRENT APPLICATION NUMBER: US/09/092,160C CURRENT FILING DATE: 1998-06-05
 SOFTWARE: PatentIn Ver. 2.1
 NUMBER OF SEQ ID NOS:
 NAME/KEY: UNSURE LOCATION: (14)..(58 OTHER INFORMATION:
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: rice expansin
 FEATURE:
 ORGANISM: Artificial Sequence
 TYPE: PRT
 178 SNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 220
 183 SNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
 123 RRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQNWQ 182
 63 VNDPQWCIKGRSIV-VTATNFC---PPGGACDPPNHHFDLSQPIYEKIALVKSGIIPVMY 118
 63 EDDPEWCIPGSIIVRYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVPVAF 122
 183 SNTYLRGOSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
178 SNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 220
 119 RRVRCKRSGGIRFTINGHSYFNLVLYTNVGGAGDVHSVSMKGSRT-KWQLMSRNWGQNWQ 177
 123 RRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQNWQ 182
 3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC 62
 3 GGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSCQKCGACFELTC 62
 63 VNDPQWCIKGRSIV-VTATNFC---PPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVMY 118
 63 EDDPEWCIPGSIIVRYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVPVAF 122
 Local Similarity
 143;
 (14)..(58)
 Conservative
 Conservative
 Xaa
 62.4%; Score 777.5; DB 4; Length 222; 64.1%; Pred. No. 4.1e-77;
 is unknown or other
 29;
 29; Mismatches 46;
 Pred. No. 4.1e-77;
 Mismatches
 46;
 Indels
 Indels
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 Gaps
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 ; ORGANISM: Lycopersicon esculentum cv. US-09-362-642-2
 US-08-845-539-2
 US-09-362-642-2
 Sequence 2, Application US/09362642 Patent No. 6350935 GENERAL INFORMATION:
 Sequence 2, Application US/08845539 Patent No. 5929303 GENERAL INFORMATION:
 Query Match
Best Local Similarity
 SEQ ID NO 2
LENGTH: 225
 Matches
 APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
 SOFTWARE:
 TYPE: PRT
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
 NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
 APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
 176
 STREET:
CITY: S
STATE:
 210
 151
 COUNTRY:
 CLASSIFICATION:
 19
 FILING DATE:
 31 GSWETAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGLSCGACFELKC 90
 APPLICATION NUMBER: US/08/845,539
 3 GGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELTC
 NWGQNWQSNTYLRGQS 191
 TNTPNWKWCLPGNPSILITATNFCPPNYALPNDNGGWCNPPRPHFDLAMPMFLKLAQYRA 150
 NWGQNWQSNAVLTGQS 225
 136;
 94111-3834
 San Francisco
 PatentIn Ver. 2.1
 California
 Two Embarcadero Center, Eighth Floor
 USA
 Conservative
 25-APR-1997
 59.0%; Score 734; DB 4; Length 225; 69.4%; Pred. No. 2.4e-72;
 Release #1.0, Version
 20;
 Mismatches
 32;
 Indels
 8;
 Gaps
 62
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 RESULT 12
US-08-845-539-6
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 ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-845-539-2
; MOLECULE TYPE: US-08-845-539-6
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 ; Patent No.
 ; Sequence 6, Application US/08845539
 Matches 136;
 Query Match
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/845
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REGISTRATION NUMBER: 34,774
 GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
NUMBER OF SEQUENCES: 8
 TELEFAX: (415) 576-03
 TELEFAX: (415) 576-030 INFORMATION FOR SEQ ID NO:
 REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 SEQUENCE CHARACTERISTICS:
 REFERENCE/DOCKET NUMBER: 02
TELECOMMUNICATION INFORMATION:
 SEQUENCE CHARACTERISTICS:
 CORRESPONDENCE ADDRESS:
 210
 176 NWGQNWQSNTYLRGQS 191
 151 GIVPVTYRRIPCRKQGGIRFTINGFRYFNLVLITNVAGAGDIIKVWVKGTKTN-WIPLSR 209
 116 GIVPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSR 175
 COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
 STREET: Two Embarca
CITY: San Francisco
STATE: California
 TYPE: amino acid TOPOLOGY: linear
 63
 31 GSWETAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGLSCGACFELKC
 / Match 58.8%; Score 732; DB 2; Local Similarity 69.4%; Pred. No. 3.9e-72;
 LENGTH: 225 amino acids TYPE: amino acid
 TELEPHONE:
 COUNTRY: USA
 91 TNTPNWKWCLPGNPSILITATNFCPPNYALPNDNGGWCNPPRPHFDLAMPMFLKLAQYRA 150
 ADDRESSEE:
 TELEPHONE:
 LENGTH:
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 94111-3834
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 Two Embarcadero Center, Eighth Floor
 Conservative
 Townsend and Townsend and Crew LLP
 (415) 576-0200
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 .5) 5, c
) 576-0300
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US-09-362-642-6
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 ; Sequence 4, Application US/08440517A
; Patent No. 5959082
 US-08-440-517A-4
 US-09-362-642-6
GENERAL INFORMATION:
APPLICANT: COSCROV
APPLICANT: GUILTIN
APPLICANT: SHCHERB.
APPLICANT: SHI, JU
 SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 6
 GENERAL INFORMATION:
 Sequence 6, Application US/09362642 Patent No. 6350935
 APPLICANT:
APPLICANT:
 Query Match
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 APPLICANT: The Regents of the University of California TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes TITLE OF INVENTION: to Control Fruit Texture and Softening FILE REFERENCE: 023070-07821005
CURRENT APPLICATION NUMBER: US/09/362,642
 NUMBER OF SEQ ID NOS:
 CURRENT FILING DATE: 1999-07-27
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 Rose, Jocelyn K.C.
 GUILTINAN,
SHCHERBAN,
SHI, JUN
 COSGROVE, DANIEL J.,
 Conservative
 55.1%; Score 685.5; DB 4; Length 179; 71.0%; Pred. No. 3.4e-67; 71.0%; Pred. No. 3.4e-67; 74.0%
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 NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
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 Sequence 4, Application US/09092160C Patent No. 6255466
 CURRENT APPLICATION NUMBER: US/09/092,160C CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER APPLICATION NUMBER: 08/060,944
 APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
 APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
 EARLIER FILING DATE: 1993-05-12
 ORGANISM: Artificial Sequence
 TYPE: PRT
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LENGTH: 227

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OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
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US-09-092-160-4
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 Database
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AAG2646483
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AAG51647
AAG51647
AAG51646
 SUMMARIES
Arabidopsis expans
Cucumber expansin-
Arabidopsis thalia
 Description
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| Rice expansi | 17 AAR94529 | 22 1 | 22 | 62.4 | .7             |
|--------------|-------------|------|----|------|----------------|
| Arabidopsis  | ш           |      | 25 |      |                |
| Arabidopsis  | <u>د</u>    |      | 25 |      | 9              |
| Arabidopsis  |             |      | 22 |      | 9              |
| Arabidopsis  | شنو         |      | 22 | •    | .9             |
| Tomato seed  | Ν           |      | 26 | ٠    | $\mathbf{\mu}$ |
| Arabidopsis  |             |      | 28 | •    | N              |
| Arabidopsis  | -           |      | 25 | •    | N              |
| Arabidopsis  | _           |      | 25 |      | N              |
| Arabidopsis  | _           |      | 25 |      | ω              |
| Arabidopsis  | μ           |      | 25 | •    | w              |
| Tomato seed  | N           |      | 25 |      | 4              |
| Arabidopsis  | _           |      | 27 | •    | 5              |
| Arabidopsis  | _           |      | 26 | •    | S              |
| Arabidopsis  | _           |      | 25 |      | ū              |
| Arabidopsis  | _           |      | 25 |      | S              |
| Arabidopsis  | ب           |      | 24 |      | S              |
| Arabidopsis  | 1           |      | 24 | -    | 5              |
| Arabidopsis  | 7           |      | 22 | 68.5 | 853            |
| Arabidopsis  | _           |      | 20 | •    | 56.            |
| Arabidopsis  | _           |      | 20 |      |                |
| Arabidopsis  | -           |      | 25 | •    | ū              |
| Arabidopsis  | _           |      | 24 | •    | S              |
| -            | 1           |      | 24 | •    | ū              |
| Rice expans  | 7           |      | 22 | •    | 5              |
| Arabidopsis  | יי          |      | 28 |      | 6              |
| Arabidopsis  | 1           |      | 28 |      | 6              |
| Arabidopsis  | سا          |      | 25 |      | 6              |
| Arabidopsis  |             |      | 25 |      | 6              |
| Arabidopsis  | -           |      | 25 |      | 9              |
| Arabidopsis  | -           |      | 25 | •    | 6              |
| Arabidopsis  | -           |      | 28 | •    | -              |
| Arabidopiis  | 1 22001     |      |    | •    | 1              |

 $\begin{array}{c} 112 \\ 123 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\ 134 \\$ 

## ALIGNMENTS

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RESULT 1
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Expansin proteins which alter the mechanical strength of poly:saccharide(s) - useful in paper mfr. and recycling
 Expansin; plant cell wall; cellulose; paper recycling; de-inking; polysaccharide.
Disclosure; Page 32; 60pp; English.
 Cosgrove DJ,
 04-APR-1996.
 Arabidopsis expansin.
 08-JUL-1996
 AAR94531;
 AAR94531 standard; Protein;
 WPI; 1996-201150/21
 (PENN-) PENN STATE RES FOUND
 12-MAY-1995;
12-MAY-1993;
 12-MAY-1994;
 AU9540262-A.
 Arabidopsis sp.
 (first entry)
 McQueen-Mason
 95US-0440517.
93US-0060944.
 94AU-0068320
 225
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 Best Loc
Matches
 Query Match
 Cucumber expansin-29 (AAR94527) is a member of a novel class of proteins that catalyse the extension of plant cell walls and the weakening of the hydrogen bonds in pure cellulose. It can be obtained by the contract of the
 Expansins are a novel class of proteins that catalyse the extension of plant cell walls and the weakening of the hydrogen bonds in pure cellulose. 2 Expansins (AAR94528 and AAR94529) have been identified rice and 3 in Arabidopsis (AAR94530-32). A cDNA clone (AAT13320)
 expansin-29; plant cell wall; cellulose;
polysaccharide; cucumber.
 coding for cucumber expansin 29 (AAR94527) has been obtd. Expancan be used e.g. in the mfr., de-inking and recycling of paper, the textile industry, to aid delignification processes, to altermechanical strength, etc.
 Claim 7;
 Cucumis sativus
 poly:saccharide(s)
 Expansin proteins which alter the mechanical
 WPI;
 (PENN-) PENN
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12-MAY-1993;
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 08-JUL-1996
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 Page 30; 60pp; English.
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 (first entry)
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93US-0060944
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Pred. No. 4.7e-124;
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 mfr.
 (see AAT13320)
 paper recycling; de-inking;
 and
 strength
 trength of recycling
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 Expansins aper, in
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 0;
 Gaps
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 60
 Or.
 in
 0;
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AAG25443
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09-MAR-1999

23-MAR-1999

25-MAR-1999

29-MAR-1999

01-APR-1999

06-APR-1999

08-APR-1999
 other host cells. Expansin proteins have also been identified in oat coleoptiles, in Arabidopsis (see AAR94530-32) and in rice (AAR94528-29), and appear to be broadly distributed throughout the plant kingdom. Expansins can be used e.g. in the mfr., de-inking and recycling of paper, in the textile industry, to aid delignification processes, to alter gel mechanical strength, etc.
 25-FEB-2000;
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 Protein identification; signal transduction pathway; metabolic pathway;
 Arabidopsis
 17-OCT-2000
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| יים הרסים הים הרטים א<br>את את א                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | PR                                              |
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| -011                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   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XX Prot
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 Query Match
Best Local Similarity
Matches 161; Conserv
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
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 Arabidopsis thaliana
 Arabidopsis
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 AAG51633;
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 16
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XX AAG5
XX AAG5
XX Prot
DE Arah
XX Prot
KW hybr
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XX
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14-OCT-1999;
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 protein identification; signal transduction pathway; metabolic
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 06-SEP-2000
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 18-OCT-2000 (first entry)
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 Local Simhes 161;
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990S-0159684

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71.2%;
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Pred. No. 1.3e-88;
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 Length 241;
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 pathway;
 Gaps
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| ים די הים הים הים הים הים הים הים הים הים הי                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | סיסים מיסים מי                                                                                                                                                                                                               |
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| 11                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 05-MAR-1999;<br>09-MAR-1999;<br>25-MAR-1999;<br>29-MAR-1999;<br>01-APR-1999;<br>08-APR-1999;<br>16-APR-1999;<br>16-APR-1999;<br>16-APR-1999;<br>21-APR-1999;<br>21-APR-1999;<br>21-APR-1999;<br>21-APR-1999;<br>23-APR-1999;<br>23-APR-1999;<br>30-APR-1999;<br>30-APR-1999;<br>06-MAY-1999;<br>06-MAY-1999;<br>06-MAY-1999; |
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Best Local Similarity 71.2%;
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Pred. No. 1.4e
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| RESULT 13  AAGS1645  AC AAGS1645;  XX AAGS1645;  XX AAGS1645;  XX AAGS1645;  XX AAGS1645;  XX The Cort-2000  XX XX Arabidopsis the cort of | 154 VSYRRVPI<br>180 NWQSNTY<br>     : <br>213 NWQSNSY                                                               |
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| קר<br>קר את הקר<br>קר את הקר                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | ק<br>אמים<br>אמים<br>אמים                                                                                           |
| 18-JUN-1999 21-JUN-1999 22-JUN-1999 23-JUN-1999 23-JUN-1999 24-JUN-1999 24-JUN-1999 25-JUN-1999 26-JUL-1999 26-JUL-1999 27-JUL-1999 28-JUL-1999 28-JUL-1999 29-JUL-1999 20-JUL-1999 21-JUL-1999 21-JUL | -1999<br>-1999<br>-1999<br>-1999                                                                                    |
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PR 27 AUG-1999 99US-0151066.
PR 27 AUG-1999 99US-0151066.
PR 27 AUG-1999 99US-0151066.
PR 27 AUG-1999 99US-0151066.
PR 28 AUG-1999 99US-0151066.
PR 29 AUG-1999 99US-0151066.
PR 29 AUG-1999 99US-0151066.
PR 20 AUG-1999 99US-0153070.
PR 10 AUG-1999 99US-0153070.
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PR 10 AUG-1999 99US-0153070.
PR 20 AUG-1999 99US-0153070.
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PR 20 AUG-1999 99US-0153070.
PR 21 AUG-1999 99US-0153070.
PR 22 AUG-1999 99US-0153070.
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PR 28 AUG-1999 99US-0153070.
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PR 20 A
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 Query Match 69.7%; Score 868; DB 21; Length 251; Best Local Similarity 67.8%; Pred. No. 6.7e-84; Matches 154; Conservative 31; Mismatches 38; Indels
 119
PVAFRRYPCEKGGGIRFTINGNPYFDLYLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWG 178
 QNWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGGF 225
 4 .
 Gaps
 84
 61
 2
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Search completed: October 11, 2002, 14:56:43 Job time: 25.9077 secs

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OM protein - protein search, using sw model
 Run on:
 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
 Total number of hits satisfying chosen parameters:
 Scoring table:
 Sequence:
 Perfect score:
 Title
 Database
 Post-processing: Minimum Match 0%
 Result
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SPTREMBL_19:*

1: sp_archea:*
2: sp_bacteria
3: sp_fungi.*
4: sp_human:
5: sp_lnwan:
6: sp_naumar
7: sp_mhc:
8: sp_org
9: sp_ph/
10: sp_r
11: sp_
13: sp
14: f
 pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
 1031.5
 1096.5
 1021.5
1020.5
1020.5
1017.5
1017.5
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1130.5
1097.5
 Score
 1023
 October 11, 2002, 14:51:00; Search time 19.5144 Seconds (without alignments) 2003.488 Million cell updates/sec
 BLOSUM62
 US-09-896-301-6
1257
 Gapop 10.0 , Gapext 0.5
 1 DYSSWQSAHATFYGGGDASG.....
 562222 seqs, 172994929 residues
 Match Length DB
97.9
97.9
89.9
87.2
84.7
84.7
82.1
81.8
81.4
81.3
81.3
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81.3
81.3
 Maximum Match 100%
Listing first 45 summaries
 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
 sp_unclassified:*
sp_rvirus:*
sp_bacteriap:*
sp_archeap:*
 sp_archea:*
 sp_bacteria:*
 sp_organelle:*
 sp_mammal:*
 sp_invertebrate:*
 sp_vertebrate:*
 sp_virus:*
 sp_rodent:*
 sp_plant:*
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082093
Q9FUM3
Q9SBT1
P93493
Q9SWY1
 P93492
Q93XP2
P93495
 Q40636
Q946J1
 Q946J0
 P93442
 Q94KT7
 SUMMARIES
 ...SNNVVPAGWQFGQTFEGGQF 226
 040636 oryza sativ
094631 oryza sativ
09467 zea mays (m
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094630 oryza sativ
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0940m3 prunus aviu
093btl fragaria an
p93493 pinus taeda
 Q93xp2
P93495
Q911b2
Q94kt3
 Description
 Q9swy1
P93492
 prunus cera
pinus taeda
zinnia eleg
 fragaria an
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|--------|--------------|-------------|--------|---------------|--------|--------|--------|-----------------|--------|--------|----------|--------|--------|----------|--------|---------|--------|------------------|--------|------------------|--------|--------|--------|--------|--------|--------|-------------|--------------|
| 910.5  | _            | 916         | 917    | 919           |        | 2      | 932.5  | ω               | 937    |        | 3        | 938.5  | 4      | 948      | 951.5  | 960.5   | 963.5  | 964.5            | 969.5  | 969.5            | 987    | 1000.5 | 002    | 003    | 800    | 1009.5 | 1010.5      | 11           |
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| 264    | 249          | 242         | 255    | 255           | 259    | 239    | 276    | 250             | 253    | 249    | 263      | 248    | 252    | 253      | 249    | 249     | 220    | 247              | 250    | 237              | 258    | 247    | 232    | 249    | 252    | 260    | 252         | 250          |
| 10     | 10           | 10          | 10     | 10            | 10     | 10     | 10     | 10              | 10     | 10     | 10       | 10     | 10     | 10       | 10     | 10      |        |                  |        |                  |        |        |        |        |        |        | 10          | 10           |
| Q9M4X6 | Q9ZP36       | Q9LLB1      | Q38866 | Q9FLC5        | Q9M4X7 | Q9ZP31 | Q94KT6 | Q9FVG9          | Q9SWD4 | Q9M5I5 | Q9ZP32   | 080622 | Q9FUM2 | 022874   | Q93XP1 | Q9LDR9  | Q9AYR1 | Q9M5I7           | Q9C554 | Q38863           | 049194 | 082625 | P93494 | Q9ZP35 | 081133 | Q9FNT0 | Q9FS30      | Q39625       |
|        |              |             |        |               |        |        |        |                 |        |        |          |        |        |          |        |         |        |                  |        |                  |        |        |        |        |        |        |             |              |
| oryza  | Azbae urcorr | ILDI Zinnia | arabta | Casca arabido | oryza  | Lycope |        | Q9fvg9 Lycopers |        |        |          |        | prunus | arabid   |        | arabido |        | Q9m51/ cripnysar |        | Q38863 arabidops |        |        | . 77   | UTCOCI | prunus | CICEL  | rs30 prunus | 9625 cucumis |
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## ALIGNMENTS

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Q40636
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Best Local :
 Matches
 Q40636
Q40636;
Q1-NQV-1996
 01-NOV-1996 (TrEMBLrel. 01, 01-DEC-2001 (TrEMBLrel. 19, EXPANSIN OS-EXP2.
 Shcherban T.Y., Shi J., Durachko D.M., Guiltinan M.J.,
McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
"Molecular cloning and sequence analysis of expansins--a highly
conserved, multigene family of proteins that mediate cell wall
extension in plants.";
Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
EMBL; U30477; AAB38074.1; "...
 Oryza sativa (Rice).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;

Ehrhartoideae; Oryzeae; Oryza.
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MEDLINE=96016146; PubMed=7568110;
 NCBI_TaxID=4530;
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 1 DYSSWOSAHATFYGGGDASGTWGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 59
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 (TrEMBLrel. 01,
 PRELIMINARY;
 Conservative
 97.9%;
 Last sequence update)
Last annotation update)
 Created)
 0;
 Score 1230.5; DB 10; Length 251; Pred. No. 2.2e-103;
 PRT;
 29E99CD57B4542B6 CRC64;
 Mismatches
 251
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 Indels
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RESULT 3
Q94KT7
ID Q94K
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 RESULT 2
Q946J1
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 Q94KT7;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
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 Eukaryota; Viridiplantae;
 Zea mays (Maize)
 ALPHA-EXPANSIN PRECURSOR.
 Q94KT7
 Curr.
EMBL;
 SEQUENCE
 Lee Y. Choi D., Kende H.;
"Expansins: ever-expanding numbers and functions.";
Curr. Opin. Plant Biol. 4:527-532(2001).
EMBL; AF394544; AAL24480.1;
 MEDLINE=21521099; PubMed=11641069;
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 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
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 Oryza sativa (Rice).
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 Q946J1
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 145 VPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWG
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 QNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF
 QNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
 VPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWG
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 DYGSWQSAHATFYGGGDASGTMGGACGYGNLYSTGYGTNTAALSTVLFNDGAACGSCYEL
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 223;
 Similarity
 PRELIMINARY;
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 251 AA;
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 (TrEMBLrel.
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 PRELIMINARY;
 26674 MW; C450366570EFE3BD CRC64;
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 Streptophyta;
 Zea.
 0;
 Score 1230.5;
Pred. No. 2.2
 Liliopsida; Poales;
 PRT;
 Mismatches
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 Embryophyta; Tracheophyta;
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 Embryophyta; Tracheophyta;
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P93442
 RESULT 4
 Matches
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 Query Match
 PRINTS; PRO1225; EXPANSNFAMLY.
PRODOM; PD002179; Pollen_allergen;
SEQUENCE 246 AA; 25898 MW; CC01
 Pfam; PF01357; Pollen_allergen; 1.
 Plant Cell 9:1661-1671(1997).
EMBL; U85246; AAB81662.1;
InterPro; IPR000882; Pollen_allergen
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
 Cho H.T
121 PVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQ 180
 MEDLINE=97480100;
 STRAIN=PIN GAEW 56; TISSUE=INTERNODE;
 NCBI_TaxID=4530;
 Oryza sativa (Rice).
 EXPANSIN.
 01-DEC-2001
 Expression of expansin genes is correlated with growth in
 SEQUENCE FROM N.A.
 01-MAY-1997
 01-MAY-1997
 P93442;
 P93442
 Signal.
 SEQUENCE
 Plant Physiol. 126:222-232(2001).
 Families in Maize.
 Wu Y., Meeley R.B., Cosgrove D.J.; "Analysis and Expression of the alpha-Expansin and beta-Expansin Gene Families in Maize ".
 MEDLINE=21249159; PubMed=11351085;
 81
 EMBL; AF332169; AAK56119.1;
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 21 YGGWQSAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGAACGSCYELR 80
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 207 QNWQSNSLLDGQSLSFQVTASDGRTVTSNGVAPAGWQFGQTFEGAQF 253
 180 QNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF
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 120 VPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWG 179
 2 YSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTYLFNDGAACRSCYELR 60
 87 RCDNNGQSCLPGTITVTATNFCPPNYGLPSDDGGWCNPPRPHFDMAQPAFLQIAQYRAGI 146
 60
 27 DYGSWQSAHATFYGGGDASGTMGGACGYGNMYSTGYGTNTAALSTALFNDGAACGSCYEL 86
 Local
 1 DYSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 59
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 RCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGI 119
 203;
 Similarity
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 (TrEMBLrel.
 (TrEMBLrel.
 253 AA;
 (TrEMBLrel.
 PRELIMINARY;
 Conservative
 PubMed=9338967;
 87.3%;
87.2%;
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26423 MW;
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 Score 1097.5; DB 10; Length 246; Pred. No. 2.2e-91;
 Last annotation update)
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 7; Mismatches
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 CC01823A37BD084F CRC64;
 7CDD5390E0104099 CRC64;
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 01-MAR-2001
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 Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Energatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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 "Expansins: ever-expanding numbers and functions.";
Curr. Opin. Plant Biol. 4:527-532(2001).
EMBL: AF934545; AAL244811; -
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EXP4.
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 Spermatophyta; Magnoliophyta; Poeae; Festuca.
 Q9FY30;
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Reidy B., McQueen-Mason S., Noesberger J., Fleming A "Differential Expression of alpha- and beta-expansin elongating leaf of Festuca pratensis.";
 STRAIN-CV, PREFEST; TISSUE-LEAF ELONGATION ZONE; MEDLINE-21377433; PubMed-11485205;
 Festuca pratensis.
Eukaryota; Viridiplantae;
 Lee Y., Choi D., Kende H.;
 EXP2
 EXPANSIN.
 SEQUENCE FROM N.A.
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 201
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 NWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
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Mismatches
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 Embryophyta; Tracheophyta;
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PA-EXP1.
 Prunus armeniaca (Apricot).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
 01-NOV-1998
 082093;
 SEQUENCE
 InterPro; IPR000882; Pollen_allergen.
PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
 Plant Mol. Biol. 46:491-504(2001).
EMBL; AJ276007; CAC06433.1; -.
 01-NOV-1998
01-DEC-2001
 082093
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ProDom; PD002179; Pollen_allergen;
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Pfam; PF01357; Pollen_allergen; 1.
 Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases EMBL; U93167; AAC33529.1; -
 Mbeguie-A-Mbeguie D.,
 STRAIN-BERGERON; TISSUE-MESOCARP PLUS EXOCARP;
 SEQUENCE
 "Molecular cloning and nucleotide strom apricot fruit.";
 SEQUENCE FROM N.A.
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 205
 85
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 25
 88
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 28
 1 DYSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL
 Local
 ы
 GQNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
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 252 AA;
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Pred. No. 2.1e
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 Mismatches
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 , Fils-Lycaon B.;
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 29;
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 Rosidae;
 Gaps
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 147
 144
 84
 59
 207
 87
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Db

208

254

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RESULT
Q9SBT1
ID
Q9
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Q9
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 Query Match
Best Local S
Matches 180
Fragaria ananassa
 Q9SBT1
Q9SBT1;
01-MAY-2000
01-MAY-2000
01-DEC-2001
 EXP2
 Yoo S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.;
"Coordinated expression of genes encoding expansins and other cell
wall-modifying enzymes is associated with pectin-related changes ir
the cell wall during ripening of cherry (P. cerasus) fruit.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF297521; AAG13982.1; -.
EMBL; AF350937; AAK48466.1; -.
Thereproceed the submitted of the submitted (FEB-2001) for the EMBL (FEB-2001) for the
 EXPANSIN.
 PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
SEQUENCE 254 AA; 27278 MW; 953A7EB2491FD0E1 CRC64;
 Wu Z., Wiersma P.A.; "Differential Expression of Expansin Genes Isolated from "Differential Expression of Expansin Genes Isolated from (Prunus avium L.) During Fruit Ripening."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
 Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids I; Rosales; Rosaceae; Amygdaloideae;
 InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
 SPECIES=P.cerasus; TISSUE=RIPENING FRUIT;
 01-MAR-2001 (TrEMBLrel. 16, 01-MAR-2001 (TrEMBLrel. 16, 01-DEC-2001 (TrEMBLrel. 19, 01)
 01-MAR-2001
01-MAR-2001
 Q9FUM3
 SPECIES=P.avium;
 SEQUENCE FROM N.A.
 Prunus avium (Cherry),
 Q9FUM3;
 SEQUENCE FROM N.A.
 NCBI_TaxID=42229, 140311;
 Prunus cerasus.
 EXP1 OR EXP2.
 EXPANSIN
 148
 208
 180 QNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
 9
 œ
 88
 60
 28
 1 DYSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL 59
 VPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGFGDVQSVSIKGSSTGWQPMSRNWG
 RCNNDPRWCRPGSIIVTATNFCPPNFAQSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGI
 RCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGI 119
 DYGGWEGAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGSCYEM
 VPVTFRRVPCMKKGGIRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQPMSRNWG
 180;
 Similarity
 (TrEMBLrel.) (TrEMBLrel. (TrEMBLrel.
 PRELIMINARY
 Conservative
 PRELIMINARY;
 (Strawberry)
 81.8%;
79.3%;
 and
 13,
13,
 Last sequence update)
Last annotation updat
 Created)
 Created)
Last sequence up
Last annotation
 Last
 Pred. No. 3.907; Mismatches
 Score 1028.5;
 PRT;
 PRT;
 253
 254
 Embryophyta;
 5; DB 10; Length .9e-85;
 ΑA
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 29;
 Prunus
 core eudicots;
 Indels
 Tracheophyta;
 Sweet
 254;
 1;
 Gaps
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 147
 87
 179
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 RESULT
 В
 QΥ
 Matches
 Query Match
Best Local
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 Query Match
 Matches 183;
 NON_TER
SEQUENCE
 "Expansins are conserved in conifers and expre exogenous auxin."
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ EMBL; U64891; AAB40635.1;
 01-MAY-1997 (TrEMBLrel. 03, 01-DEC-2001 (TrEMBLrel. 03, EXPANSIN (FRAGMENT).
 ProDom; PD002179; Pollen_allergen; 1.
 InterPro; IPR000882; Pollen_allergen. Pfam; PF01357; Pollen_allergen; 1.
 Eukaryota; Viridiplantae; Streptophyta; Eml
Spermatophyta; Coniferopsida; Coniferales;
 P93493
 PRINTS; PRO1225; EXPANSHFAMLY.
PRINTS; PRO1225; EXPANSHFAMLY.
PRODOM; PD002179; Pollen_allergen; 1.
PROSITE; PS00626; RCC1_2; UNKNOWN_1.
SEQUENCE 253 AA; 26887 MW; CE39CF(
 PRINTS; PR01225; EXPANSNFAMLY.
 P93493;
 InterPro; IPR000882; Pollen_allergen
InterPro; IPR000408; RCC1.
Pfam; PF01357; Pollen_allergen; 1.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Rosoideae; Fragaria.
 SEQUENCE FROM
 NCBI_TaxID=3352;
 Pinus taeda (Loblolly pine).
 Plant Physiol. 12:1273-1279(1999).
EMBL; AF159563; AAF21101.1; -.
 STRAIN-CV.
 TISSUE-HYPOCOTYL;
 independent."
 "An expansin
 Civello P.M., Sabehat A.,
 SEQUENCE FROM N.A
 206
 179
 146
 119
 10
 98
 59
 Local Similarity
 N
 26
 ட
YSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYELR
 cal Similarity
178; Conser
 LRCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHEDMAEPAFLQIGVYRAG 118
 DY-SSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYE 58
 GQNWQSNNYLNGQALSFQVTTSDGRTVTSNNVAPGNWQFGQTFSGGQF
 GQNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
 MRCDNDPRWCLPGSIIVTATNFCPPNFAQANDNGGWCNPPLQHFDLAEPAFLQIAQYRAG
 DYGAGWVGGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGSCYE 85
 232 AA;
 CHANDLER;
 Conservative
 Conservative
 PRELIMINARY;
 gene expressed in ripening
 N.A.
 24745 MW;
 81.3%;
79.1%;
 81.4%;
80.3%;
 UNKNOWN_1.
MW; CE39CF00ADEA1CEF CRC64;
 Powell A.L.T., Bennett A.B.;
 13;
 18;
 , Diaz-Sala C., Greenwoo conifers and expressed
 Last sequence update)
Last annotation update)
 Created)
 Score 1021.5;
Pred. No. 1.5e-
 Score 1023; DB 10
Pred. No. 1.2e-84;
 PRT;
 1340B0573DE907CF CRC64;
 Mismatches
 Mismatches
 232
 Embryophyta;
es; Pinaceae;
 strawberry fruit is
 AΑ
 DB 10;
 Greenwood M.S.;
 DB 10;
-84;
 28;
 30;
 databases
 Indels
 Indels
 Length
 in response
 Length
 Tracheophyta; Pinus.
 253
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 Gaps,
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RESULT 11
Q9SWY1
ID Q9SWY
AC Q9SWY
AC Q9SWY
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 Matches
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 P93492; PRELIMINARY;
P93492;
01-MAY-1997 (TrEMBLTel. 03, C.
01-MAY-1997 (TrEMBLTel. 03, L.
01-DEC-2001 (TrEMBLTel. 19, L.
 Pinus
 EXPANSIN (FRAGMENT)
 Interpro; IPRO00882; Pollen_allergen. Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNFAMLY. PRODOM; PD002179; Pollen_allergen; 1. SEQUENCE 253 AA; 27150 MW; 2675BB:
 response to exogenous auxin.";
Plant Physiol. 120:827-832(1999).
EMBL; AF085330; AAD47901.1; -
 TISSUE-HYPOCOTYL;
MEDLINE-99329318; PubMed-10398718;
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 208
 181 NWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQ 225
 Hutchison K.W., Singer P.B., McInnis S., "Expansins are conserved in conifers and
 SEQUENCE FROM N.A.
 NCBI_TaxID=3352;
 Pinus taeda (Lobiolly pine).
 EXPANSIN
 09SWY1;
 Q9SWY1
 121
 88 CNDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIV 147
 61 CDNDGQWCLPGSYTYTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGIV 120
 187
 181
 127
 121 PVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQ 180
 Toca I
 2 YSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYELR 60
 67
 61
 PILYTRYPCLRKGGIRETVNGHSYENLVLITNVGGAGDVHAVSIKGSRSGWQPMSRNWGQ 207
 NWQSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSNWQFGQTFEGSQ 252
 PVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQ 180
 YGGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMR 87
 taeda
 178;
 NWQSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSNWQFGQTFEGSQ 231
 NWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQ 225
 PILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVHAVSIKGSRSGWQPMSRNWGQ 186
 CDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGIV 120
 CNDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIV 126
 YGGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMR
 Similarity
(Loblolly pine)
 Conservative
 PRELIMINARY;
 81.3%; Score 1021.5; DB 10; Length 253; 79.1%; Pred. No. 1.7e-84;
 18;
 Last
 Last annotation update)
 Created)
 PRT;
 Mismatches
 2675BB1569BD75D4 CRC64;
 sequence update)
 232 AA
 253
 Diaz-Sala C., Greenwood expressed in hypocotyls
 B
 28; Indels
 Greenwood M.S.;
 1; Gaps
 1;
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Вb
 B
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 RESULT 13
 В
 Matches 182;
 Query Match
 Matches
 Query Match
 YOO S.-D., Gao Z., Cantini C., Loescher W., van Nocker S., "Coordinated expression of genes encoding expansins and other cell wall-modifying enzymes is associated with pectin-related changes in the cell wall during ripening of cherry (P. cerasus) fruit."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosales; Rosaceae; Amygdaloideae; Prunus.
 Q93XP2;
 SEQUENCE
 TISSUE=RIPENING FRUIT;
 SEQUENCE FROM N.A
 NCBI_TaxID-140311;
 Prunus cerasus
 EXP1
 EXPANSIN
 01-DEC-2001
01-DEC-2001
 01-DEC-2001
 SEQUENCE
 exogenous auxin.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U64890; AAB40634.1; ...
 NON_TER
 PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
 187
 InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
 Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.; "Expansins are conserved in conffers and expressed in response
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
 26
 181 NWQSNSYLDGQSLSEQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQ 225
 121 PVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQ 180
 TISSUE=HYPOCOTYL;
 SEQUENCE FROM N.A.
 NCBI_TaxID=3352;
 1 DY-SSWOSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLENDGAACRSCYE 58
 Local Similarity
 67
 61 CDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEDAFLQIGVYRAGIV 120
 7 YGGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMR 66
 Local
 2 YSSWOSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYELR 60
DYGGGWEGGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGSCYE 85
 NWQSNSYLNGQSLSFQVTTSDGRTIVSNNVAPSNWQFGQTFEGSQ 231
 PILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVHAVSIKGSMSGWQPMSRNWGO
 CNDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIV
 177;
 Similarity
 253 AA;
 Conservative
 232 AA; 24734 MW; 1340AF483DE0741F CRC64;
 (TrEMBLrel. 19, Created)
(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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 Conservative
 26861 MW;
 81.1%;
79.8%;
 81.2%; Score 1020.5; 78.7%; Pred. No. 1.86
 13; Mismatches
 W; 9C24484F14AA52CD CRC64;
 19; Mismatches
 Pred. No.
 Score 1019;
 253
 2.8e-84;
 DB 10; Length 253;
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 . 8e-84
 DB 10; Length 232;
 31;
 28; Indels
 core eudicots; Rosidae;
 <u>ب</u>
 1; Gaps
 Gaps
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 <u>..</u>
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Qy

59 LRCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAG 118

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RESULT 14
P93495
 Ъ
 QΥ
 В
 Qy
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 QΥ
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 В
 Qy
 Ъ
 Qy
 Вb
 Qy
 Q9LLB2
 RESULT 15
 Matches 177;
 Query Match
Heliantheae; Zinnia.
 P93495;
01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
EXPANSIN (FRAGMENT)
 InterPro; IPR000882; Pollen_allergen. pfam; PF01357; Pollen_allergen; 1. pRINTS; PR01225; EXPANSNEAMLY. proDom; PD0002173; Pollen_allergen; 1.
 exogenous auxin.";
submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases
EMBL; U64893; AAB40637.1;
 Eukaryota; Viridiplantae; Stre
Spermatophyta; Coniferopsida;
 P93495
 Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S.; "Expansins are conserved in conifers and expressed in response to
 Q9LLB2;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
 Pinus taeda (Loblolly pine)
 119 IVPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNW 178
 SEQUENCE
 NON_TER
 TISSUE=HYPOCOTYL;
 SEQUENCE FROM N.A.
 NCBI_TaxID=3352;
 206
 179 GONWOSNSYLDGOSLSFOVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
 Zinnia elegans.
 Q9LLB2
 187
 181 NWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQ 225
 127 PILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVNAVSIKGSRSGWQPMSRNWGQ 186
 121 PVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQ 180
 61 CDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHEDMAEDAELQIGVYRAGIV 120
 67
 Local Similarity
 7 YGGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMO 66
 2 YSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYELR 60
 NWQSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSNWQFGQTFEGSQ 231
 232 AA;
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 Conservative
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 80.9%; Score 1017.5; DB 78.7%; Pred. No. 3.4e-84;
 Streptophyta; Embryophyta; Tracheophyta;
ida; Coniferales; Pinaceae; Pinus.
 19; Mismatches
 PRT;
 232 AA
 245 AA.
 DB 10; Length 232;
 28; Indels
 1;
 Gaps
 145
 1;
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OX RN RN RP RA RT DR DR DR DR DR
 Qy
 В
 QΥ
 DЬ
 Qy
 B
 В
 Matches 176;
 Query Match
 Best
 Im K.H., Cosgrove D.J., Jones A.M.;
Im K.H., Cosgrove D.J., Jones A.M.;
"Subcellular localization of expansin mRNA in xylem cells.";
"Subcellular localization of expansin mRNA in xylem cells.";
Plant Physiol. 123:463-470(2000).
EMBL; APE330332; AAPE35901.1;
EMBL; APE330332; AAPE3591.1;
Pfon; PF01357; Pollen_allergen; 1.
 PRINTS; PRO1225; EXPANSNEAMLY.
ProDom; PD002179; Pollen_allergen;
SEQUENCE 245 AA; 26201 MW; F661
 SEQUENCE FROM N.A. MEDLINE=20317189; PubMed=10859177;
 NCBI_TaxID=34245;
 SEQUENCE
 181 NWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
 140 PISFQRVPCVKKGGVRFTINGHSYFNLILITNVGGAGDVHSVSIKGSKTGWQSMSRNWGQ
 200
 121 PVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQ 180
 80
 61 CDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGIV 120
 Local
 20 YGGWENGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGSCYEMR 79
 2 YSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTYLFNDGAACRSCYELR 60
 Similarity
 Conservative
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2002, 14:59:42
 21; Mismatches
 F66E26114C27E360 CRC64;
 28; Indels
 1; Gaps
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Search completed: October 11, Job time: 20.5144 secs

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GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: October 11, 2002, 14:50:30; Search time 5.83764 Seconds (without alignments) 1499.000 Million cell updates/sec

Title: Perfect score: US-09-896-301-6 1257

1 DYSSWQSAHATFYGGGDASG.....SNNVVPAGWQFGQTFEGGQF 226

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| ω<br>ω     | 32         | 31                 | 30                 | 29                 | 28                 | 27         | 26                 | 25         | 24         | 23         | 22         | 21         | 20         | 19         | 18         | 17         | 16        | 15                 | 14         | 13         | 12         | 11         | 10         | 9          | 80         | 7          | o,         | տ          | 4          | ω                  | N          | _                  |                                       | Result  |
|------------|------------|--------------------|--------------------|--------------------|--------------------|------------|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|-----------|--------------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|------------|--------------------|------------|--------------------|---------------------------------------|---------|
| 80         | 81         | 81                 | 81                 | 81                 | 81                 | 81         | 81                 | 81         | 81.5       | 81.5       | 82.5       | 82.5       | 82.5       | 83         | 83.5       | 83.5       | 84        | 84.5               | 85         | 86.5       | æ          | 90.5       | 92.5       | 93         | 105.5      | 175        |            | 203        | 206.5      |                    | 214.5      | 232                |                                       | SCOTE   |
| 6.4        | 6.4        | 6.4                | 6.4                | 6.4                | 6.4                | 6.4        | 6.4                | 6.4        | 6.5        |            |            |            | 6.6        |            |            |            |           |                    | 6.8        |            |            | 7.2        | 7.4        | 7.4        |            |            |            | 16.1       | 16.4       | 16.5               | 17.1       | 18.5               |                                       | Query   |
| 677        | 1173       | 474                | 456                | 444                | 444                | 442        | 433                | 430        | 3695       | 1376       | 1193       | 574        | 574        | 571        | 747        | 513        | 3011      | 1176               | 571        | 1246       | 766        | 333        | 646        | 418        | 242        | 263        | 263        | 191        | 265        | 269                | 263        | 246                |                                       | anath n |
| ы          | ۳          |                    |                    |                    |                    |            |                    |            | ш          |            | Н          |            | ۲          | ب          | ш          | Н          | ب         | ب                  | ب          | ب          | Н          | _          | ب          |            | ب          | Н          | ш          | μ          | ب          | r                  | _          | ٢                  | è                                     | Ħ       |
| SP87_DICDI | TSP1_XENLA | SHU1_ECOLI         | SHU7_ECOLI         | SHU5_ECOLI         | SHU4_ECOLI         | SHU3_ECOLI | SHU6_ECOLI         | SHU2_ECOLI | LMA5_HUMAN | CRBH_HUMAN | LMG2_HUMAN | FLB3_CAMJE | FLA3_CAMJE | FLB1_CAMJE | GUND_CELFI | GUX1_TRIVI | POLG_HCV1 | C1CB_BACTG         | FLA1_CAMJE | YMV2_CAEEL | DPP4_HUMAN | CATJ_MOUSE | NA95_HUMAN | GUN2_TRIRE | GUN5_TRIRE | MPO1_ORYSA | MPP1_PHLPR | MPZ1_MAIZE | MPH1_HOLLA | MPA1_PHAAQ         | MPL1_LOLPR | MPC1_CYNDA         | + + + + + + + + + + + + + + + + + + + | T)      |
| dictyost   | 10         | P09745 escherichia | P09751 escherichia | P09749 escherichia | P09748 escherichia |            | P09750 escherichia | esche      | homo       |            | homo sapie | campylobac | campylobac |            |            | trichoder  |           | P56953 bacillus th |            |            | home       |            |            |            | tricho     | oryza sati | ч          | zea may    | holcus la  | Q41260 phalaris ag | lolium per | 004701 cynodon dac |                                       |         |

δõ

3 SSWQSAHATFYGG---GDASGTMGGTCGYGNLYSTGYTN-TAALSTVLFNDGAACRSCYE 58

| 45                 | 44         | 43         | 42                 | 41        | 40         | 39         | 38         | 37        | 36                 | 35                 | 34                 |   |
|--------------------|------------|------------|--------------------|-----------|------------|------------|------------|-----------|--------------------|--------------------|--------------------|---|
| 78                 | 78.5       | 78.5       | 78.5               | 78.5      | 79         | 79.5       | 79.5       | 79.5      | 80                 | 80                 | 80                 |   |
| 6.2                | 6.2        | 6.2        | 6.2                | 6.2       | 6.3        | 6.3        | 6.3        | 6.3       | 6.4                | 6.4                | 6.4                |   |
| 213                | 1286       | 642        | 513                | 181       | 213        | 2437       | 1385       | 852       | 3718               | 1429               | 703                |   |
| 1                  | _          | _          | μ                  | <b>—</b>  | <u> </u>   | _          | سا         | سا        | ۳                  | _                  | فسإ                |   |
| XYNA_BACCI         | AIDA_ECOLI | NA95_MOUSE | GUX1_TRIRE         | GUN_MYTED | XYNA_BACSU | NOTC_BRARE | YMS5_CAEEL | CSG_HALHA | LMA5_MOUSE         | LI12_CAEEL         | COAT_SMSV4         |   |
| P09850 bacillus ci |            |            | P00725 trichoderma |           |            |            | _          | _         | Q61001 mus musculu | P14585 caenorhabdi | P36285 san min r l | - |

## ALIGNMENTS

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 01-APR-1990 (Rel. 14, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pollen allergen Lol p 1 precursor (Lol p I) (Allergen R7).
Lolium perenne (Perennial ryegrass).
 This
 -!- SUBCELLULAR LOCATION: Secreted.
-!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
-!- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
 I allergenic determinant.";
Mol. Immunol. 26:557-561(1989).
 proteins from rye-grass (Lolium perenne)
and efficient purification method.";
biochem. J. 234:305-310(1986).
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Poeae; Lolium.
 MPL1_LOLPR
P14946; P1
 Esch R.E., Klapper D.G.;
"Isolation and characterization of a
 MEDLINE=89364850; PubMed=2475768;
 SEQUENCE OF 236-263
 Cottam G.P., Moran D.M., Standring R.;
"Physicochemical and immunochemical characterization of allergenic
 MEDLINE=86242068; PubMed=3718469;
 SEQUENCE OF 24-53.
 rye-grass
 "Cloning and sequencing of Lol pI, the major allergenic protein of
 Avjoglu A., Davies
 MEDLINE=91160716; PubMed=2001733;
 TISSUE=Pollen
 SEQUENCE FROM N.A.,
 allergen
 Perez M., Ishioka G.Y., Walker L.E., Chesnut R.W., "CDNA cloning and immunological characterization o
 SEQUENCE FROM N.A. MEDLINE=90375479; PubMed=1697854;
 NCBI_TaxID=4522;
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 LOLPR
 183
 167
 123
 114
 242
 216
 76
 59
 16
 Biol. Chem. 265:16210-16215(1990).
 LQFG
 R.B.;
 --VYRAGIVPVSYRRVPCVKKGGIRFTIN----GHSYFNLVLVTNVAGPGDVQSVSIK-G
SWISS-PROT entry is
 -QFG
 DSDEFIPMKSSWGAIWRIDPKKPLKG-PFSIRLTSEGGAHLVQDDVIPANWKPDTVYTSK
 SSTGWQPMSRNWGQNWQ--SNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGW------
 DKLRKAGELTLQFRRVKCKYPSGTKITFHIEKGSNDHYLALLVKYAAGDGNIVAVDIKPR
 IKCKEPVE-CSGEPVLVKIT---
 LRCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIG-----
 SKWLEARATFYGSNPRGAAPDDHGGACGYKDVDKPPFDGMTACGNEPIFKDGLGCRACYE
 P19964;
 ĭ.J.,
 101
 245
 218
 pollen
 279:210-215(1991).
 p I."
 Smith P.M., Pollock J., Theerakulpisut P., ries S., Hough T., Singh M.B., Simpson R.J., Ward L.D.
 STANDARD;
 AND SEQUENCE OF 24-48
 copyright.
 PRT;
 It is produced through a collaboration
 major cross-reactive grass group
 -DKNYEHIAAYHFDLSGKAFGAMAKKGQE
 263
 pollen prepared by
 of the
 rye
 a rapid
 grass
 182
 166
 75
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В
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 Qy
 MPA1_PHAAQ
 RESULT 3
 Query Match
Best Local
 Matches
 PIR; A23341; A23341.
PIR; B37881; B37881.
PIR; S13614; S13614.
HSSP; P43214; 1WHO.
 CONFLICT
 CARBOHYD
VARIANT
 01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Major pollen allergen Pha a 1 precursor (Pha
 InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
 the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contents to the content is not removed.
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 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
 SEQUENCE
 CONFLICT
 VARIANT
 VARIANT
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 DOMAIN
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 SIGNAL
 Allergen;
 PROSITE; PS50843; EXPANSIN_CBD; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1
 EMBL;
 EMBL; M57474; AAA63279.1;
 or send an email to license@isb-sib.ch).
 between the Swiss Institute of Bioinformatics
 147
 114
 207 DKWIELKESWGAVWRIDTPDKLTG-PFTVRYTTEGGTKSEFEDVIPEGWK 255
 101
 62
 41
 σ
 G-WQPMSRNWGQNWQSNS--YLDGQSLSFQVAVSDGRTVTSNNVVPAGWQ
 VYRAGIVPVSYRRVPCVKKGGIRFTINGHSYFN----LVLVTNVAGPGDVQSVSIKGSST
 WQSAHATFYGGGDASGTM--GGTCGYGNLYSTGYTN-TAALSTVLFNDGAACRSCYELRC 61
 PHAAQ
 VRSAGELELQFRRVKCKYPDDTKPTFHVEKASNPNYLAILVKYVDGDGDVVAVDIKEKGK
 TKP-ESCSGEAVTVTIT---
 DNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRP-HFDMAEPAFLQI------G 113
 WLDAKSTWYGKPTGAGPKDNGGACGYKNVDKAPFNGMTGCGNTPIFKDGRGCGSCFEIKC
 M57474; AAA63279.1; -. M57476; AAA63278.1; -.
 67;
 Similarity
 Glycoprotein;
 263 AA;
 Conservative
 24
61
181
32
68
177
210
246
28
 STANDARD;
 263
167
262
32
68
177
210
246
28
31
 28438 MW;
 29.1%;
 17.1%;
 Signal; Multigene family.
 32;
 N '> D.
A '> G.
F '> V.
F '> C.
 Pred.
 Score
 N-LINKED (GLCNAC.
 EXPANSIN-LIKE CBD.
 POLLEN ALLERGEN LOL
 PRT;
 7675896F279C88C9
 Mismatches
 -DDNE--EPIAPYHFDLSGHAFGSMAKKGEEQN 146
 > C (IN REF. 3).
> C (IN REF. 3).
> WW (IN REF. 3)
 No.
 214.5;
 269
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 DB 1;
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 CRC64;
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Spermatophyta; Magnoliophyta; Poeae; Phalaris.

Liliopsida;

Embryophyta;

Poales;

Poaceae;

Tracheophyta;

Suphioglu C., Singh

MEDLINE=96105569; PubMed=8564724;

TISSUE=Pollen; SEQUENCE FROM N.A. NCBI\_TaxID=28479; Phalaris aquatica (Canary grass). Eukaryota; Viridiplantae; Streptophyta;

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 CARBOHYD
CONFLICT
 MPH1_HOLLA STANDARD;
P43216; Q39975;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
01-MAR-2002 (Rel. 41, Last ann
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 PROSITE; PS50843; EXPANSIN_CBD; 1. PROSITE; PS50842; EXPANSIN_EG45; 1.
 PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
 "Cloning, sequencing and four isoforms of
 Major pollen allergen Hol 1 1 precursor (Hol
 SEQUENCE
 SIGNAL
 MEDLINE-93319091; PubMed-7687099;
 SEQUENCE OF 30-49.
 pollen
Holcus lanatus (Velvet grass).
 HOLLA
 DOMAIN
 InterPro; IPR000882; Pollen_allergen.
 "Cloning,
 213
 153
 114 VYRAGIVPVSYRRVPCVKKGGIRFTIN----GHSYFNLVLVTNVAGPGDVQSVSIKGSST
 107
 0102)
 62
 47
 Local
 5 WOSAHATFYGGGDASGTM--GGTCGYGNLYSTGYTN-TAALSTVLFNDGAACRSCYELRC
 G-WQPMSRNWGQNWQSNS--YLDGQSLSFQVAVSDGRTVTSNNVVPAGWQ 216
 SKP-ESCSGEPITVHIT------DDNE--EPIAPYHFDLSGHAFGSMAKKGEEEN
 DNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRP-HFDMAEPAFLQI-----G
 WLDAKSTWYGKPTGAGPKDNGGACGYKDVDKAPFNGMTGCGNTPIFKDGRGCGSCFELKC
 DKWIELKESWGAIWRIDTPDKLTG-PFTVRYTTEGGTKAEFEDVIPEGWK
 VRGAGELELQFRRVKCKYPDGTKPTFHVEKGSNPNYLALLVKYVDGDGDVVAVDIKEKGK
 P43214; 1WHO
 PF01357; Pollen_allergen; 1.
 S80654; AAB35984.1; -
 65;
 Similarity
 Glycoprotein;
 Allergy
 Conservative
 25:853-865(1995).
 16.5%;
 29011 MW;
 and
 Last sequence up
 Signal.
 expression in Escherichia coli of Pha a a 5, the major allergens of canary grass
 34;
 N-LINKED
 Pred.
 Score
 EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
 MAJOR POLLEN ALLERGEN PHA A
 PRT;
 05883A458ACE877F CRC64;
 Mismatches
 207.5; DB 1
 ED (GLCNAC.
 265
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 DB 1;
 1 I) (Hol 1 1.0101
 98;
 Indels
 Length
 33,
 allergens
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Query Match
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Matches 64
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 MEDLINE-96319506; PubMed-8768803; Schlaak M., Be Schramm G.D., Petersen A., Bufe A., Schlaak M., Be "Identification and characterization of the major grass (Holcus lanatus), Hol 1 1 and Hol 1 5."; Int. Arch. Allergy Immunol. 110:354-363(1996).
 "Mapping of IgE-binding epitopes on the recombinant major group allergen of velvet grass pollen, rHol l l.";
J. Allergy Clin. Immunol. 99:781-787(1997).
 Schramm G.D., Bufe A., E Submitted (NOV-1993) to
 STRAIN-CV.
 SEQUENCE FROM N.A
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
 SEQUENCE
 EMBL; Z27084; CAA81610.1; -. EMBL; Z68893; CAA93121.1; -.
 entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 STRAIN-CV.
 Schramm G.D.,
 MEDLINE=97358126; PubMed=9215246;
 STRAIN-CV
 SEQUENCE OF 18-265 FROM N.A.
 Poeae; Holcus
 VARIANT
 DOMAIN
 CHAIN
 Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNFAMLY.
 DOMAIN
 SIGNAL
 Allergen;
 InterPro; IPR000882; Pollen_allergen.
 HSSP; P43214; 1WHO.
 PROSITE;
 PROSITE;
 ProDom; PD002179;
 170
 149
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 62
 5
 SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN. SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
G-WQPMSRNWGQNWQSNS--YLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFE
 WQSAHATFYGGGDASGTM--GGTCGYGNLYSTGYTN-TAALSTVLFNDGAACRSCYELRC
 LRSAGELELKFRRVKCKYPDGTKPTFHVEKGSNPNYLALLVKYIDGDGDVVAVDIKEKGK
 WLDAKSTWYGKPTGAGPKDNGGACGYKDVDKPPFSGMTGCGNTPIFKDGRGCGSCFETKC 102
 VYRAGIVPVSYRRVPCVKKGGIRFTIN----GHSYFNLVLVTNVAGPGDVQSVSIKGSST
 TKP-ESCSGEPVTVHIT-------DDNE--EPIAPYHEDLSGHAFGSMAKKGEEQK 148
 DNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRP-HFDMAEPAFLQIG----- 113
 64; Conserv
 PS50843;
PS50842;
 Signal.
 26
63
183
103
265
 AVENEAE;
 AVENEAE;
 AVENEAE; TISSUE=Pollen;
D., Bufe A., Becker W.M.,
 Conservative
 Bufe A., Petersen A., Haas H.,
 EXPANSIN_EG45; 1
 Pollen_allergen;
 EXPANSIN
 265
265
169
264
 TISSUE-Pollen;
 TISSUE-Pollen;
 16.4%;
27.1%;
 28590
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X
 39;
 Score 206.5;
Pred. No. 9.7e
39; Mismatches
 EMBL/GenBank/DDBJ databases
 EXPANSIN-LIKE CBD.
T -> S (IN HOL L 1.0102).
 MAJOR POLLEN ALLERGEN HOLEXPANSIN-LIKE EG45.
 POTENTIAL.
 1FE23B3EE198AD6D
 Schlaak
 .7e-11;
 DB 1;
 100;
 Schlaak M., Becker W.M.;
 Becker W.M.;
 CRC64;
 Length
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 DOMAIN
 MAIZE
 ProDom; PD002179; Pollen_allergen; 1.
PROSITE; PS50843; EXPANSIN_CBD; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
 MPZ1_MAIZE Q07154;
 Allergen; Multigene family.
 Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNFAMLY.
 MaizeDB; 65840;
 HSSP;
 EMBL; L14271; AAA33496.1;
 rye
 Broadwater A.H.,
 MEDLINE=94010312; PubMed=8406014;
 SEQUENCE FROM N.A.
 NCBI_TaxID=4577;
 Zea mays (Maize)
 InterPro;
 204 TVTSNNVVPAGWQ
 209
 G
 48
 99
 39
 DISEASE: CAUSES MAIZE POLLEN ALLERGY.
SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLESIMILARITY: CONTAINS I EXPANSIN-LIKE EG45 DOMAIN.
SIMILARITY: CONTAINS I EXPANSIN-LIKE CBD DOMAIN.
 DEVELOPMENTAL STAGE:
 131:227-230(1993).
TISSUE SPECIFICITY: POLLEN TISSUE.
 grass.
 POLLEN MITOSIS
 TAALSTVLFNDGAACRSCYELRCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPP
 JC1524; JC1524.
 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation -
 AVLVKFVADDGDIVLMEIQDKLSAEWKPMKLSWGAIWRMDTAKALKG-PFSIRLTSESGK
 LVLVTNVAGPGDVQSVSIKGS-STGWQPMSRNWGQNWQSNS--YLDGQSLSFQVAVSDGR
 APYHFDLSGKAFGSLAKPGLNDKLRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGCNPNYV
 TACGNVPIFKDGKGCGSCYEVRCKEKPE-CSGNPVTVFITDM-
 DKWIELKESWGAVWRVDTPDKLTG-PFTVRYTTEGGTKGEAEDVIPEGWKADTAYE 263
 RP-HFDMAEPAF--
 P43214; 1WHO.
 Similarity
 the maize homolog of the allergen-encoding Lol pl gene of
 IPR000882; Pollen_allergen.
 105
191 /
 Conservative
 Andropogoneae;
 AA;
 STANDARD;
 Rubinstein A.L.,
 186
 21362 MW;
 16.1%;
 1 (Zea m I).
 Last sequence update)
Last annotation update)
 Created)
 --LQIGVYRAGIVPVSYRRVPCVKKGGIRFTINGHSYFN----
 EXPRESSION LOW
 29;
 Score 203; DB
Pred. No. 1.4e
29; Mismatches
 Zea.
 EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
; 6E2A9DF921C45C63 CRC64;
 PRT;
 Chay C.H., Klapper D.G.,
 191
 DB 1; 1
1.4e-10;
hes 75;
 BEFORE
 AA
 OF ALLERGENS DOMAIN.
 AND
 Length 191;
 Indels
 HIGH
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 Gaps
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 MPP1_PHLPR
 RESULT
 Query Match
Best Local
 Matches
 DOMAIN
DOMAIN
 Pfam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
Probom; PD002179; Pollen_allergen;
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pollen allergen Phl p 1 precursor (Phl p I).
 SEQUENCE
 EMBL; X78813; CAA55390.1; -. HSSP; P43214; IWHO.
 Scheiner O.,
 PHLPI.
Phleum pratense (Common timothy)
 CARBOHYD
 SIGNAL
 Allergen;
 PROSITE; PS50843;
 or send an email to license@isb-sib.ch).
 MEDLINE=95015525; PubMed=7930302;
 SEQUENCE FROM N.A.
 NCBI_TaxID=15957;
 MPP
 PROSITE; PS50842; EXPANSIN_EG45;
 InterPro;
 167 KVIAKDIIPANWR 179
 101
 6
 62
 41
 σı
 TKP-EACSGEPVVVHIT-
 PHLPR
 63;
 Similarity
 Glycoprotein;
1 23
 IPR000882; Pollen_allergen.
 Valenta R., V
 263 AA;
 Conservative
 24
61
181
 STANDARD;
 EXPANSIN_CBD;
 263
167
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32
 28457 MW;
 16.0%;
26.7%;
 Vrtala
 39;
 N-LINKED (GLCNAC
 Pred.
 Score
 POTENTIAL
 s.
 PRT;
 Mismatches
 No.
 201.5;
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 "Complementary DNA cloning of the major allergen Phl p I from timothy grass (Phleum pratense); recombinant Phl p I inhibits IgE binding to
 -i- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS
-i- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-i- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
 Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Pooldeae; Poeae; Phleum.
 entities requires a license agreement (See http://www.isb-sib.ch/announce/
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 VYRAGIVPVSYRRVPCVKKGGIRFTIN----GHSYFNLVLVTNVAGPGDVQSVSIKGSST 169
 WQSAHATFYGGGDASGTM--GGTCGYGNLYSTGYTN-TAALSTVLFNDGAACRSCYELRC 61
LRSAGELELQFRRVKCKYPEGTKVTFHVEKGSNPNYLALLVKYVNGDGDVVAVDIKEKGK
 DNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRP-HFDMAEPAFLQIG----- 113
 WLDAKSTWYGKPTGAGPKDNGGACGYKDVDKPPFSGMTGCGNTPIFKSGRGCGSCFEIKC 100
 Signal; Multigene family.
 EXPANSIN-LIKE CBD.
 EXPANSIN-LIKE EG45
 POLLEN ALLERGEN PHL
 046BA249C17BC048 CRC64;
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 DB 1;
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170 G-WOPMSRNWGONWOSNS--YLDGOSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFE 222

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RESULT
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 Matches
 Query Match
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 01-MAR-2002 (Rel. 41, Last sequence update)
Major pollen allergen Ory s 1 precursor (Ory s
Oryza sativa (Rice).
 MPO1_ORYSA
Q40638;
 _ORYSA
 EMBL;
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 SIGNAL
 --- DISEASE: CAUSES GRASS POLLEN ALLERGY.
--- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS
---- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE E045 DOMAIN.
---- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
 "Cloning, expression and immunological characterization of Ory s the major allergen of rice pollen."; Gene 164:255-259(1995).
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoldeae; Oryzeae; Oryza.
 proDom; pD002179; pollen_allergen; 1.
proSITE; pS50843; EXPANSIN_CBD; 1.
proSITE; pS50842; EXPANSIN_EG45; 1.
 InterPro; IPR000882; Pollen_allergen Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNFAMLY.
 Bhalla P.L.;
 MEDLINE=96069591; PubMed=7590339;
 SEQUENCE FROM N.A.
 SEQUENCE
 CARBOHYD
 or send an email to license@isb-sib.ch).
 entities
 NCBI_TaxID=4530;
 DOMAIN
 119
 DOMAIN
 207
 134 GIRETIN----GHSYFNLVLVTNVAGPGDVQSVSIK-GSSTGWQPMSRNWGQNWQSNS--
 82
 61
 23
 TISSUE SPECIFICITY: EXPRESSED IN MATURE ANTHERS VEGETATIVE OR OTHER FLORAL TISSUES.
 SUBCELLULAR LOCATION: Secreted.
 DKWIELKESWGAIWRIDTPDKLTG-PFTVRYTTEGGTKTEAEDVIPEGWKADTSYE 261
 GGTCGYGNLYSTGYTN-TAALSTVLENDGAACRSCYELRCDNDGQWCLPGSVTVTATNLC
 ----NDE-----PIAAYHFDLSGLAMAKDGKDEELRKAGIIDTQFRRVKCKYPA
 PPNYALPNDDGGWCNPPRP----HFDMAEPAFLQIG-----VYRAGIVPVSYRRVPCVKKG
 GGACGYKDVDKAPFLGMNSCGNDPIFKDGKGCGSCFEIKCSKP-EACSDKPALIHVTDM-
 U31771; AAA86533.1; -. P43214; IWHO.
 Theerakulpisut P.,
 Similarity
 requires a license agreement (See http://www.isb-sib.ch/announce/
 Glycoprotein; Signal; Multigene family.
 263 AA;
 24
61
178
32
 Conservative
 STANDARD;
 23
263
164
259
 28497
 13.9%;
=
 MW.
 Goulding
 37;
=
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 Score 175; DB 1;
Pred. No. 4.7e-08;
7; Mismatches 82;
 EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC.
 MAJOR POLLEN ALLERGEN ORY
 EXPANSIN-LIKE
 POTENTIAL
 B1C5F24EA398DD60 CRC64;
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 263
 Suphioglu C.,
 (Ory s I).
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 EG45.

 Length 263;
 Indels
 BUT
 (POTENTIAL)
 Singh M.B.,
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 34;
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 Gaps
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 Query Match
Best Local
 Matches
 TRIRE
 JI NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase (Cellulase V) (EG V).
 CARBOHYD
DISULFID
DISULFID
 ACT_SITE
ACT_SITE
DOMAIN
 Trichoderma reesei (Hypocrea jecorina)
Eukaryota; Fungi; Ascomycota; Pezizomyc
 01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last send
15-DEC-1998 (Rel. 37, Last and
Endoglucanase V precursor (EC
 P43317;
01-NOV-1995
 InterPro; IPR000254; CBD_fungal.
InterPro; IPR000334; Glyco_hydro_45.
Pfam; PF00734; CBD_1; 1.
Pfam; PF02015; Glyco_hydro_45; 1.
ProDom; PD001821; CBD_fungal; 1.
 This
 STRAIN=QM9414 / RUT C-30; MEDLINE=95075308; PubMed=
 SEQUENCE FROM N.A.
 GUN5_TRIRE
 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 modified and this statement is not removed.
 the European Bioinformatics Institute. The use by non-profit institutions as long
 -
 isolated by expression in yeast."; Mol. Microbiol. 13:219-228(1994).
 EMBL; Z33381; CAA83846.1; -. HSSP; P00725; 2CBH.
 Saloheimo A., Henrissat B., Hoffren A.-M.,
 NCBI_TaxID=51453;
 SEQUENCE
 DOMAIN
 DOMAIN
 CHAIN
 SIGNAL
 Cellulose
 PROSITE;
 SMART; SM00236; fCBD;
 between
 "A novel
 Hypocreales; Hypocreaceae; Hypocrea.
 164
 224
 8
3 SSWQSAHATFYGG------GDASGTMGGTCGYGN-LYSTGYTNTAALSTVLFND-----
 HYDROLASES).
SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING
 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 linkages in cellulose.
SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45
 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation
 PLKG-PFSVRVTTEGARRSSAEDAIP 248
 DTKITFHIEKASNPNYLALLVKYVAGDGDVVEVEIKEKGSEEWKALKESWGALWKIDTPK 223
 YLDGQSLSFQVAVSDGRTVTSNNVVP 212
 Similarity
 PS01140;
 PS00562; CBD_FUNGAL; 1.
 PS50842;
 small endoglucanase gene, egl5,
 18
27
134
18
183
206
182
213
224
 Conservative
 STANDARD;
 PubMed-7984103;
 EXPANSIN_EG45; 1
 242
27
134
182
205
242
182
230
240
 24411 MW;
 18;
 Pred.
 ВY
 PRO/SER-RICH (LINKER).
CELLULOSE-BINDING (BY SIMILARITY).
 Score 105.5;
 N-LINKED (GLCNAC. .
 CATALYTIC
 PROTON DONOR
 NUCLEOPHILE (BY SIMILARITY)
 ENDOGLUCANASE V.
 Pezizomycotina;
 PRT;
 CC033FC51326C71D CRC64;
 Mismatches
 SIMILARITY
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 242 AA
 There are no restrictions ong as its content is in
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 from Trichoderma reese
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 DB 1;
 Teleman O.,
 Usage
 46;
 Sordariomycetes,
 SIMILARITY).
 .) (POTENTIAL)
 Length
 Indels
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 Penttilae
 and
 DOMAIN (CBD).
 OF GLYCOSYL
 242;
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RESULT
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 Вb
 InterPro; IPR000254; CBD_fungal.
InterPro; IPR001547; Glyco_hydro_F5
Pfam; PF00734; CBD_1; 1.
 use by non-profit institutions as long modified and this statement is not removed.
 This
 "Identification of an essential glutamate residue in the active of endoglucanase III from Trichoderma reesei."; FEBS Lett. 316:137-140(1993).
 01-AUG-1988 (Rel. 08, Createu, 01-AUG-1988 (Rel. 08, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) Findroalucanase EG-II precursor (EC 3.2.1.4) (E
 P07982;
01-AUG-1988
 SMART;
 EMBL;
 or send
 entities requires a
 the
 Saloheimo M., Lehtovaara P., Penttilae M., Teeri T.T., Staahlberg J. Johansson G., Pettersson G., Clayssens M., Tomme P., Knowles J.K.C.; "EGIII, a new endoglucanase from Trichoderma reesei: the characterization of both gene and enzyme.";
 ProDom;
 Pfam; PF00150; cellulase; 1.
 HSSP;
 [1]
SEQUENCE FROM N.A.
 Macarron R., v
Claeyssens M.;
 MEDLINE=93131031;
 ACTIVE SITE GLU-350
 MEDLINE=88255850; PubMed=3384334;
 NCBI_TaxID=51453;
 Hypocreales;
 Eukaryota; Fungi; Ascomycota; Pezizomycotina;
 Trichoderma reesei (Hypocrea jecorina)
 121
 101
 G
 70
 50
 16
 s SWISS-PROT entry is copyright. It is produced through ween the Swiss Institute of Bioinformatics and the En European Bioinformatics Institute. There are no restrictly by non-profit institutions as long as its content
 HYDROLASES).

SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN
CAUTION: WAS ORIGINALLY CALLED ENDOGLUCANASE EG-III.
 FUNCTION: THE BIOLOGICAL CONVERSION OF CELLULOSE TO GLUCOSE GENERALLY REQUIRES THERE TYPES OF HYDROLYTIC ENZYMES:
(1) ENDOGLICANASES WHICH CUT INVERNAL BETA-1, 4-GLUCOSIDIC BONDS;
(2) EXOCELLOBIOHYDROLASES THAT CUT THE DISSACCHARIDE CELLOBIOSE FORM THE NONREDUCING END OF THE CELLULOSE POLYMER CHAIN;
 linkages in cellulose.
SIMILARITY: BELONGS TO CELLULASE FAMILY A
 CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
 ; M19373; AAA34213.1;
S28372; S28372.
; P00725; 2CBH.
 VGGTNQYGYSYHFDI----MAQNEIFGDNVV-VDFEPIAC 155
 TRIRE
 CGAGCGKCYQLTSTGQAPCSSCGTGGAAGQSIIVMVTNLCP----NNGNAQWC----PV
 SAYKATTTRYYDGQEGACGCGSSSGAFPWQLGIGNGVY----TAAGSQALFDTAGASW
 -GAACRSCYELR----
 s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
 BETA-1,4-GLUCOSIDASES WHICH HYDROLYZE THE CELLOBIOSE SHORT CELLO-OLIGOSACCHARIDES TO GLUCOSE.
 PD001821;
 van
 ----HFDMAEPAFLQIGVYRAGIVPVSYRRVPC
 Hypocreaceae;
 STANDARD;
 Beeumen
 CBD_fungal; 1.
 PubMed=8093602;
 -CDNDGQWCLPG-SVTVTATNLCPPNYALPNDDGGWCNPPRP-
 J.,
 Hypocrea.
 Henrissat B.,
 PRT;
 418
 de
 (Endo-1,4-beta-glucanase)
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 Matches
 O9ULX6; Q9UGMO; Q9NRQO; O94792;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Neighbor of A-kinase anchoring protein 95 (Homologous to AKAP95
 MOD_RES
CARBOHYD
DISULFID
DISULFID
 TISSUE=T-cell lymphoma, and Placenta; MEDLINE=20347256; PubMed=10748171; Westberg C., Yang J.-P., Tang H., Red
 Orstavik S., Eide T., C
Jahnsen T., Skalhegg B.
 MEDIINE=20163008; PubMed=10697960;
Seki N., Ueki N., Yano K., Saito T., Masuho Y., Muramatsu M.-A.;
"cDNA cloning of a novel human gene NAKAP95, neighbor of A-kinase anchoring protein 95 (AKAP95) on chromosome 19p13.11-p13.12 region.";
 HUMAN
 ACT_SITE
 DOMAIN
DOMAIN
 protein,
 SEQUENCE FROM N.A. MEDLINE=20222332;
 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
 PROSITE;
 SEQUENCE FROM
 Biol.
 protein) (HA95) (Helicase A-binding protein 95)
 "Identification, cloning and characterization of a novel nuclear
 TISSUE=Fetal brain;
 SEQUENCE FROM N.A.
 NCBI_TaxID=9606;
 NA95_HUMAN
 SEQUENCE
 DOMAIN
 CHAIN
 SIGNAL
 Cellulose
 128
 183
 128
 91
 56
 89
 11
 Local
 8 AHATEYGGGDASGTMGGTCGYGNLYSTGYTNTAALSTVLENDGAACRSCYELRCDNDGQW 67
 QSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQF 217
 AASILYGGAVAQQTVWGQC--GGIGWSGPTNCA-----PGSACSTLNPYYAQ-----
 -SNNYPDGIGQMQHFVNEDGMTIFR---LPVGWQY 158
 PCVKKGGIRFTINGHSYFNLVLVTNVAG-----PGDVQSVSIKGSSTGWQPMSRNWGQNW 182
 CIPGATTIT-TSTRPPSGPTTTTRATSTSSSTP
 CLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGIVPVSYRRV 127
 Similarity
C., Yang J.-P., Tang H., Reddy T.R., V shuttle protein binds to RNA helicase
 HA95, homologous
ll 92:27-37(2000).
 PS00562; CBD_FUNGAL; 1.
PS00659; GLYCOSYL_HYDROL_F5; 1.
 protein 95 (AKAP95)
enet. 45:31-37(2000).
 degradation;
 418
 Conservative
 Eide T.,
 N.A.
 homologous to
 STANDARD;
 PubMed=10761695;
 21
418
57
91
418
22
124
46
56
239
350
 44227
 23.3%;
 Collas
 .s.;
 7.48;
 Hydrolase;
 --GVNIAGEDEGCTTDGTCV---TSKVYPPLKNFTG---
 W.
 21;
 Pred. No. v.,v
21; Mismatches
 Þ.,
 A-kinase
 Craniata; Vertebrata; Catarrhini; Hominidae
 Score 93;
 NUCLEOPHILE
 BY SIMILARITY.
BY SIMILARITY.
 N-LINKED (GLCNAC. .
 PROTON DONOR (BY SIMILARITY)
 PYRROLIDONE CARBOXYLIC
 LINKER
 CELLULOSE-BINDING
 PRT;
 26A492D55237A49B CRC64;
 Han
Reddy T.R., Wong-Staal F.;
RNA helicase A and activates
 Glycosidase;
 I.O.,
 anchoring
 .76;
 DB 1;
 Hominidae;
 Tasken
 72;
 Length 418,
 Glycoprotein; Signal.
 (BY SIMILARITY).
 (HAP95)
 protein 95.
 K., Kieff E.,
 Euteleostomi;
 (POTENTIAL)
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 "Selection system for genes encoding nuclear-targeted proteins.";
Nat. Biotechnol. 16:1338-1342(1998).
-!- FUNCTION: COULD PLAY A ROLE IN CONSTITUTIVE TRANSPORT ELEMENT (CTE) -MEDIATED GENE EXPRESSION. DOES NOT SEEM TO BE IMPLICATED THE HINDING OF REGULATORY SUBUNIT II OF PKA.
-!- SUBCULIVAR LOCATION: NUCLEAR AT STEADY STATE BUT SHUTTLES BETWIND NUCLEUS AND CYTOPLASM.
 SEQUENCE
 CONFLICT
 DOMAIN
 Nuclear protein; Zinc-finger
 SMART; SM00355; ZnF_C2H2; 1
 EMBL; AJ243467; CAB65092.1; -.
EMBL; AF199414; AAF8648.1; -.
EMBL; AB015332; BAA34791.1; ALT_INIT
InterPro; IPR000822; Znf-C2H2.
 EMBL;
 or send an email to license@isb-sib.ch).
 TISSUE-Fetal
 SEQUENCE OF 1-358 FROM N.A.
 DOMAIN
 DOMAIN
 DOMAIN
 175
 169
 119
 120
 73
 60
 18
 Local
 Biol. Chem.
 2 YSSWQSAHATFYGGGD-ASGTMGGTCGYGNLYSTGYTNTAALSTVLFNDGAACRSCYEL- 59
MFQGMRGGGAFPGG
 VPVSYRRVPCVKKGGIRFTI-----NGHSYFNLVLVTNVAGPGDVQS----VSIKGSS 168
 --AGWOFGQTFEGG
 ----GERYDSYESCDSRAVLSERDLYRSGYDYSELDPEMEMAYEGQYDAYRDQFRMRGND
 SSDTNANTSASGSASADSV-LSRINQRL---
 RCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGI 119
 TFGPRAQGWARDARSGRPMASGYGRMWEDPMGARGQCMS--
 YSDTSAQPTCDYGYGTWNSGTNRGYEGYGYGYGYGQDNTTN----YGYGMATSHSWEMP
 AB025905; BAA85003.1; -.
 Similarity
 constitutive transport element.";
hem. 275:21396-21401(2000).
 646 AA;
 362
391
484
41
 ·GW-----QPMSRNWGQNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVP---
 Conservative
 610
 brain;
 640
 71648 MW;
 23.68;
 7.48;
 29;
 Score 92.5;
 D -> N (IN REF. 3).
S -> N (IN REF. 3).
ALTTODEN -> EFSWGAWC (IN REF. 4).
H -> Q (IN REF. 2 AND 3).
EEEKEQEEAEGGALDEGAQGEAAGISEGAEGYPAQPPYPPE
 NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
C2H2-TYPE.
 LPCPQSQP (IN REF. 3).
EEEEEGAVPLLGGALQRQIRGIPGLDVEDDEE
RGPCWEGRCNARSAASRASTWRTTRKK (IN
 Pred.
 C2H2-TYPE.
TYR/GLY-RICH.
 PA -> RRRRSRRRLRAVPWTRGRRAKRQGFRRAQRACRRS
 PRO-RICH
 EED855A81BB06585 CRC64;
 Mismatches
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 DΒ
 -DMVPHL---ETDMMQGGVYGSG-
 108;
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 -GASRLPSLFSQNIIPEYG
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 SHUTTLES BETWEEN
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RESULT CATJ_MO
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 Matches
 Q9R014; Q9WV51;
16-OCT-2001 (Rel
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_MOUSE
CATJ_N
 ACT_SITE
ACT_SITE
ACT_SITE
DISULFID
DISULFID
DISULFID
DISULFID
 CARBOHYD
CONFLICT
 Hydrolase;
SIGNAL
 PROSITE;
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 Sol-Church K., Frenck J., Troeber D., Mason R.W.; "Cloning of a mouse cysteine protease."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases -:- SUBCELLULAR LOCATION: Lysosomal (Potential).
 SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUE=Embryo;
MEDLINE=99456833; PubMed=10526153;
 Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
 16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Cathepsin J precursor (EC 3.4.22.-) (Cathepsin P) (Cathro-p).
 CHAIN
 or send an
 SEQUENCE FROM
 Tisljar K., Deussing J., Peters C.; "Cathepsin J, a novel murine cysteine
 CTSJ OR CTSP.
 EMBL; AF136272; AAF13142.1; EMBL; AF158182; AAD41898.1;
 entities
 STRAIN-C57BL/6;
 SEQUENCE
 CARBOHYD
 CARBOHYD
 CARBOHYD
 PROPEP
 PROSITE;
 PRINTS; PR00705;
 Pfam; PF00112;
 InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; Thiolprot_act_site.
 MEROPS;
 HSSP; P07711;
 TISSUE SPECIFICITY: EXPRESSED IN PLACENTA. SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN PAPAIN FAMILY OF THIOL PROTEASES.
 MOUSE
 a
 MGI:1349426;
l Similarity
57; Conser
 placenta-restricted expression.
ett. 459:299-304(1999).
 C01.038; -
 and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).
 PS00640;
 PS00639;
 PS00139;
 Thio
 333
 (Rel.
Conservative
 N.A
 1CJL.
 AA;
 Peptidase_C1;
 STANDARD;
 TISSUE-Placenta;
 protease;
 PAPAIN
 Ctsj.
 THIOL_PROTEASE_HIS;
THIOL_PROTEASE_HS;
 37147
 25.0%;
 Created)
 MW.
16;
 Glycoprotein; Lysosome; Zymogen; Signal
 BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
BY SIMILARITY.
CHARLED (GLCNAC...
N-LINKED (GLCNAC...)
P-> PK (IN REF. 2).
 Score 90.5;
Pred. No. 0.
 CATHEPSIN
 BY SIMILARITY.
 ACTIVATION PEPTIDE
 POTENTIAL.
 PRT;
 F9A8FF1D5A13B721
 SIMILARITY.
 Mismatches
 333 AA
 protease of the papain family
 . 98;
 DB
 1.
 84;
 CRC64;
 Length 333;
) (POTENTIAL)
) (POTENTIAL)
 (POTENTIAL)
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 TISSUE-Peripheral Diou.,
MEDLINE-92325476; pubMed=1352530;
Tanaka T., Camerini D., Seed B., Torimoto Y.,
Tanaka T., Camerini D., Seed B., Morimoto C.;
Tanaki T., Schlossman S.F., Morimoto C.;
Tanaki T., Schlossman S.F., Morimoto C.;
 01.AUG-1992 (Rel. 23, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dipeptidyl peptidase IV (EC 3.4.14.5) (DPP IV) (T-cell activation antigen CD26) (TP103) (Adenosine deaminase complexing protein-2)
 "Cloning CD26.";
 peptidase
Biochim. I
 MEDLINE=95012454; PubMed=7927537;
Abbott C.A., Baker E., Sutherland G.R., McCaughan G.W.
"Genomic organization, exact localization, and tissue
the human CD26 (dipeptidyl peptidase IV) gene.";
Immunogenetics 40:331-338(1994).
"Dipeptidyl peptidase IV (CD 26) gene expression in enterocyte-like colon cancer cell lines HT-29 and Caco-2. Cloning of the complete human coding sequence and changes of dipeptidyl peptidase IV mRNA levels during cell differentiation.";
 Trotot P., Barbat A.;
 Darmoul
 MEDLINE=92165847;
 TISSUE=Colon;
 SEQUENCE OF 1-551 FROM N.A
 MEDLINE=93171637;
 SEQUENCE FROM N.A.
 TISSUE=Placenta,
 SEQUENCE
 Misumi Y., Hayashi Y., Arakawa F., Ikehara Y.;
"Molecular cloning and sequence analysis of human dipeptidyl peptidase IV, a serine proteinase on the cell surface.";
Biochim. Biophys. Acta 1131:333-336(1992).
 SEQUENCE
 NCBI_TaxID=9606;
 Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Primates;
 (ADABP).
DPP4 OR ADCP2 OR CD26.
 DPP4_HUMAN P27487;
 Tanaka T.;
 MEDLINE=92329551;
 270
 143
 214
 102
 173
 115
 ISSUE-L
 47
 Н
 Immunol.
 Immunol.
 sapiens
 GNKG--CQSGTAHQAFEYVLKNKG------LEAEAT----YPYEGKDG---
 FNDGAACRS-----CYELRCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPH
 DYKDWREEGYVTPVRNQGKCGSCWAFAAAGAIEGQMFWKT--GNLTPLSVQNLLDCSKTV
 DYSSW-QSAHAT------FYGGGDASGTMGGTCGYGNLYSTGYTNTAALSTVL
 SYFVNHAVLVVGYGSEGDV-----KDGNNYWL-IKNSWGEEWGMNGYM
 SYF--NLVLYTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQNWQSNSYL
 SENASANITDYVNLPPNELYLWVAVASIGPVSAAIDASHDSFR
 FDMAE----
 D.,
 FROM N.A.
 FROM
 149:481-486(1992)
 Lacasa
 150:2090-2090(1993).
 (Human)
 N.A.
 STANDARD;
 PubMed=1347043;
a M., Baricault
 PubMed=1352704;
i Y., Arakawa F.,
 PubMed=8094732;
 -PAFLQIGVYRAGIVPV---
 Craniata; Vertebrata; Catarrhini; Hominidae;
 PRT;
 Ē.,
 Torimoto Y., Dang N.H.,
 Marguet
 766
 A
 Hominidae;
 cell activation antiger
 D.,
 SYRRVPCVKKGGIRFTINGH
 Sapin
 -FYNGGIYYEPNCS
 Euteleostomi;
 188
 expression
 C.,
 Kameoka
 -PCRYR
 J.
 of.
 269
 142
 101
 46
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"Isolation of a cDNA probe for the hum dipeptidylpeptidase IV and assignment chromosome 2.";
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 "Human dipeptidyl peptidase IV gene promoter: tissue-specific regulation from a TATA-less GC-rich sequence characteristic of housekeeping gen promoter.";
Biocham T 217.000
 entities requires a or send an email to
 Morrison M.E., Vijayasaradhi S., Houghton A.N.;
 MEDLINE-93210468; PubMed-8096237;
 TISSUE=Kidney;
 Biochem. J.
 MEDLINE=96067599;
 SEQUENCE OF 1-31 FROM N.A
 Ann. Hum. Genet.
 MEDLINE=91024044; PubMed=1977364;
 TISSUE-Colon;
 SEQUENCE OF 545-766
 J. Biol. Chem.
 PARTIAL SEQUENCE.
 8
 PTM: THE SOLUBLE FORM (SDPP) DERIVES FROM BY PROTEOLYTIC PROCESSING.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY S'
 POLYPEPTIDE
SUBUNIT: HOP
 DATABASE: NAME=PROW;
 A SOLUBLE FORM.
PTM: THE SOLUBLE FORM
 SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO
 WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd26.htm".
 PROLYL OLIGOPEPTIDASE FAMILY
 email to license@isb-sib.ch).
 311:835-843(1995).
 HOMODIMER
 267:4824-4833(1992).
 54:191-197(1990)
 PubMed=7487939;
 FROM
 N.A.
 NOTE=CD guide CD26
 for the human
 Engelstein D.,
 Swallow D., Trugnan human intestinal
 (See http://www.isb-sib.ch/announce/
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 YMV2_CAEEL
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YMV2_CAEEL STANDARD; PRT; 1246 AA. P34504; P34505; P34506; P90907; 01-FEB-1994 (Rel. 36 Created) 30-MAY-2000 (Rel. 39, Last sequence update) 01-MAR-2002 (Rel. 41, Last annotation update) Hypothetical 130.6 kDa protein K04H4.2 in chromosome III.
 569
 155 GPGDVQSVSIKGSSTGWQ 172
 SEQUENCE
 CARBOHYD
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 InterPro; IPR002469; DPPIV_N_term.
InterPro; IPR000379; Est_lip_thioest_actsite.
InterPro; IPR001375; Peptidase_S9.
InterPro; IPR002471; Prol_endopep_ser.
Pfam; PF00930; DPPIV_N_term; 1.
Pfam; PF00936; Peptidase_S9; 1.
PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
 529 ILP--PHFDKSKKYPLLLDVY-AG------PCSQKADTVFRLNWATY-----LA 568
 469 QLRCSGPGLPLYTLHSSVNDKGLRVLEDNSALDKMLQNVQMPSKKLDFIILNETKFWYQM 528
 416 YYISNEYKGMPGGR----NLYKIQLSDYTKVTCLSCELNPERCQYYSVSFSKEA---KYY 468
 ACT_SITE
 DOMAIN
 TRANSMEM
 DOMAIN
 Hydrolase; Aminopeptidase; Dipeptidase; Serine protease; Transmembrane; Glycoprotein; Signal-anchor.
 97 --PPRPHEDMAEPAFLQIGVYRAGIVPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVA 154
 58 ELRCDNDG--QWCLPGSYTYTATNLCPPNYALP------96
 12 FYGGGDASGTMGGTCGYGNLYS---TGYTNTAALS-----TVLFNDGAACRSCY 57
 Tecal
 STENIIVASFDGRGSGYQ 586
 U13732; AAB60646.1; JOIN
U13733; AAB60646.1; JOIN
U13734; AAB60646.1; JOIN
W1777; AAA51943.1;
M17477; AAA52308.1;
M60536; AAA52308.1;
X60708; CAA43118.1;
X60708; CAA43118.1;
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 ; $09.003; -
 Similarity
 437
557
663
766 AA;
 Conservative
 CDHU26.
 88278 MW;
 6.98;
 JOINED.
 20; Mismatches
 N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
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 N-LINKED
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K -> R (I
V -> I (I
 Score 87;
Pred. No.
 CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
CHARGE RELAY SYSTEM (BY SIMILARITY).
 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN). EXTRACELLULAR (POTENTIAL).
 SOLUBLE FORM OF DPP (SDPP) (BY SIMILARITY).
 CYTOPLASMIC (POTENTIAL).
 MEMBRANE FORM OF DPP (MDPP).
 -> R (IN
 (GLCNAC. . .) (POTENTIAL)
 REF.
 DB 1; Length 766;
 66; Indels
 64;
 Gaps
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SON ON SERVICE TO THE SERVICE OF THE
Query Match
Best Local Similarity
Matches 50; Conserv
 EMBL; 227078; CAA81587.1; -.
EMBL; 227078; CAA81588.1; -.
PIR; 540992; 540992;
PIR; 540993; 540994;
PIR; 540994; 540994.
HSSP; P10968; 2CWG.
 SEQUENCE
 Durbin R.;

Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.

-i- ALTERNATIVE PRODUCTS: 2 ISOFORMS; K04H4.2A (SHOWN HERE) AND K04H4.2B; ARE PROBABLY PRODUCED BY ALTERNATIVE SPLICING.
 SMART; SM00494; ChtBD2; 1.
SMART; SM00289; WR1; 14.
 WormPep; K04H4.2A; CE19967.
WormPep; K04H4.2B; CE19968.
InterPro; IPR002557; Chitin_binding.
InterPro; IPR002899; EB.
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
 Hypothetical
 entities requires a license agreement (See http://www.isb-slb.ch/announce/or send an email to license@isb-slb.ch).
 use by non-profit institutions as long modified and this statement is not removed.
 Wilson R., Ainscough R., Anderson K., Baynes C., Berks M., Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulsun A. Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulsun A. Fraser A., Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N., Jahrer J., Lightning J., Lloyd C., Mortimore B., O'Callaghan M., Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen J. Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R., Waterston J., Thierry Mieg J., Thomas K., Vaudin M., Vaughan K., Watson R., Watson R., Watson A., Weinstock L., Wilkinson-Sproat J.,
 REVISIONS
 elegans
 STRAIN=BRISTOL N2;
MEDLINE=94150718; PubMed=7906398;
 Nature 368:32-38(1994).
 Eukaryota; Metazoa; Nematoda; Chromadorea
Rhabditidae; Peloderinae; Caenorhabditis.
 Caenorhabditis elegans
 ^{2}.2 Mb of contiguous nucleotide sequence from chromosome III of C ^{1}eans.":
 SEQUENCE FROM N.A.
 K04H4.2
 1246
 | protein;
| 166 | 529
 AΑ;
 6.9%; Score 86.5;
23.3%; Pred. No. 8
 130610 MW;
 Nematoda; Chromadorea; Rhabditida; Rhabditoldea;
 Alternative splicing.
 EASANFPDSDPARFSSYSCGCMG -> VG
 GLHCDTAINLCCPLLLPLTDPKNPKKRKTERRKQKQDGNEM
 GNGLMALSIPVHCSLSDDCPIASRCEYGKCCPFLSESADST
 ISOFORM KO4H4.
 DSDTNSTTNPSQPETTKTKNNTKKSNSSKKHRKPKKKDVDP
 SSECPIGSVEVDPRFGTSCRYSLQCPSPYFCNQRGQ
 STORCDLHTLCPPDFTCSLSGKCCKLNIHCPDGTVPETSCQ
SASNHDHCPSSSHKCTLLNKEHFACCYSPGLVVEGSVTAEV
 ANCTSDEDCPTTFKCYQGCCKLAVCPRSLTAVKFTCKTQYH
CRANEHCFFGGCCPKTIELAVIKSQVLTMSKDNEHTKETEK
LIIGDCEVDTRVKKCDIDIICPEMSECVDGICCKQPPKARC
 LSDPLLQNDFPTGPPGYGFPEHLSNLDEVLTRAQCDGECPA
 (IN ISOFORM KO4H4.2B)
 SDSVGETTPVIIKEEIISTATKVWKKVDKTSGVSINKNKCL
 ITPTPTRTTEPPKLRCLSSNTDEVNSLGGASSSSATCGGTN
 4FA1A17D3F9606C4 CRC64;
 There are no rest
 DB 1;
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 Length 1246;
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Conservative

16;

Pred. No. 8.8;

Mismatches

82;

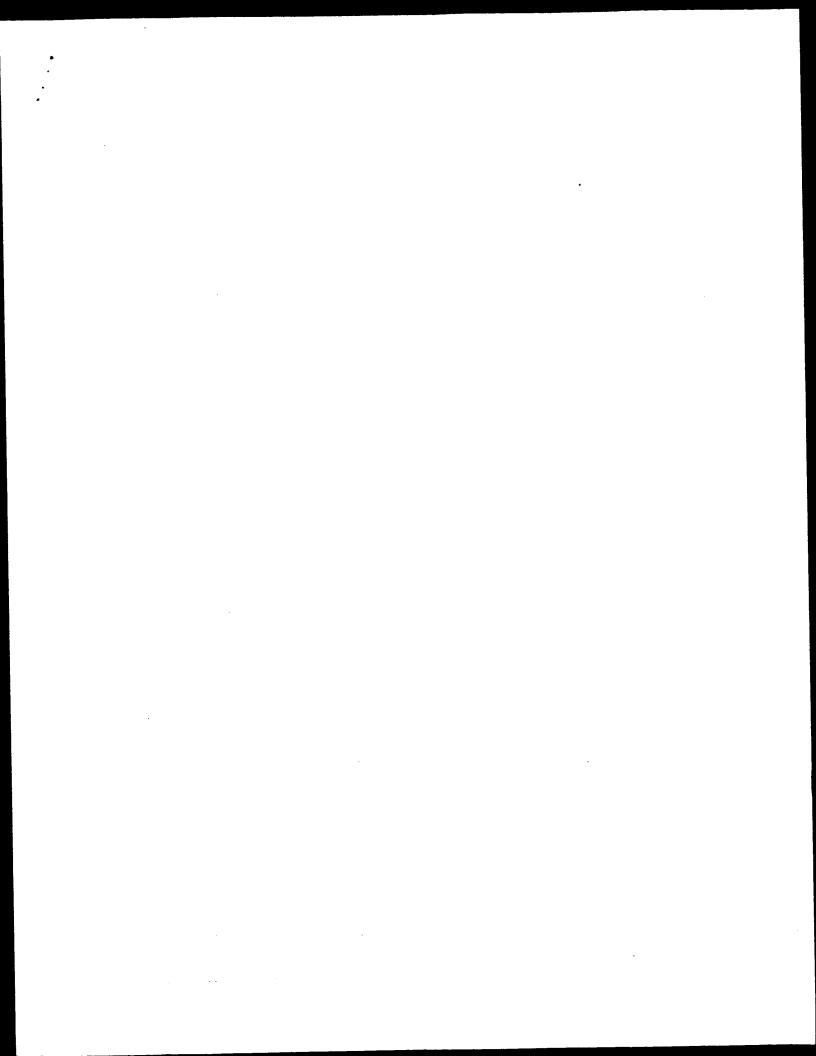
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 MEDLINE-20150912; PubMed-10688204; Parkhill J., Wren B.W., Mungall K., Ketley J.M., Churcher C., Parkhill J., Wren B.W., Mungall K., Ketley J.M., Feltwell T., Holroyd S. Basham D., Chillingworth T., Davies R.M., Feltwell T., Holroyd S. Jagels K., Karlyshev A.V., Moule S., Pallen M.J., Penn C.W., Quail M.A., Rajandream M.A., Rutherford K.M., van Vliet A.H.M.,
 P56963; Q9PMW0;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
 [1]
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
 Bacteria; Proteobacteria; epsilon subdivision; Campylobacter group;
 CAMJE
 Campylobacter
 Campylobacter jejuni
 FLAA OR CJ1339C
 Flagellin A
 FLA1_CAMJE
 modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
 FORM THE FILAMENTS OF BACTERIAL FLAGELLA.
-!- SUBUNIT: HETEROPOLYMER OF FLAA AND FLAB.
-!- SIMILARITY: BELONGS TO THE BACTERIAL FLAGELLIN FAMILY.
 Whitehead S., Barrell B.G.; "The genome sequence of the food-borne pathogen Campylobacter jejuni
 NCBI_TaxID=197;
 130 VKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQNWQSNSYLD 189
 824 AGGCVNGQCGTGYTCSNGLCCAGTSTTVKCLDGSDAVGACIP-SCTGDGCGGVQVSYYCG 882
 or send an email to license@isb-sib.ch).
 the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
 This SWISS-PROT entry is copyright. It is produced through a collaboration
 -1- FUNCTION: FLAGELLIN IS THE SUBUNIT PROTEIN WHICH POLYMERIZES
 Nature 403:665-668(2000)
 reveals hypervariable sequences."
 947 GYSLTNGVCCP--ASVTCTDEISIGPCTGTGFNGG 979
 190 GQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGG 224
 883 SG-YTCTTGNICCPINSCPN--GGEV-----LGPTINGLCPTGY----
 SEQUENCE
 PRINTS; PR00207; FLAGELLIN.
proDom; PD000316; Flagellin_C; 1.
 EMBL; AL139078; CAB73766.1;
 Flagella; Complete proteome.
INIT_MET 0 0
 InterPro; IPR001029; Flagellin_C.
InterPro; IPR001492; Flagellin_N.
 393
49 DGAAC-----RSCYELRCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPH 101
 Local Similarity
 N
 PGSVTVTATNICPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGIVPVSYRRVPC 129
 ASGIMGGICGYGNLYSIGYINIAALSIVLFNDGA-ACRSCYELRCDNDG------QWCL 69
 YSS-VSAYMSSAGSGFSSGS-GYSVGSGKNYSTGFANAIAISAASQLSTVYNVSAGSGFS 450
 YSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGYTNTAA-----LSTVL-----FN 48
 non-profit
 the Swiss Institute of Bioinformatics
 571 AA;
 Conservative
 TVQGNLCCSATCTDGSTGLPSVNGVCI----
 STANDARD;
 58907 MW;
 6.8%; score 85; DB.1 23.4%; Pred. No. 5.1; tive 26; Mismatches
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 9C63B2A10C1AE863 CRC64;
 571 AA
 DB.1; Length 571;
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 Db
 Query Match
Best Local
 Matches
 P5693;
P5693;
90-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
90-MAY-2000 (Rel. 39, Last annotation update)
Crysticidial crystal protein cry1Cb (Insecticidal delta-endotoxin pesticidial crystal protein cry1Cb (Insecticidal delta-endotoxin cry1Cb)) (Crystaline entomocidal protoxin) (133 kDa crystal protein).
CRYICB OR CRYIC(B).
CRYICB OR CRYIC(B).
 thuringlensis galleriae.";
Appl. Environ. Microbiol. 59:1131-1137(1993).
-i- FUNCTION: PROMOTES COLLOIDOSMOTIC LYSIS BY BINDING TO THE MIDGUT
 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
 Bacillus/Staphylococcus group; Bacillus. NCBI_TaxID=29338;
 C1CB_BACTG
 451 SGSTLSQFATMKTTAFGVKDETAGVTTLKGAMAV-----
 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
 "Cloning a novel cryIC-type gene from a strain of Bacillus
 Kalman S.S.
 MEDLINE=93236401; PubMed=8476286.
 STRAIN=HD-29
 SEQUENCE FROM N.A.
 530 IRDVDFAAESANYSKAN----ILAQSGSYAMAQANSVQ 563
 159 VQSVSIKGSSTGWQPMSRNWGQNWQSNSYLDGQSLSFQ 196
 485 MDIAETAITNLDQIRADI------GSVQNQVT--STINNITVTQVNVKAAESQ 529
 102 FDMAEPAFLQIGVYRAGIVPVSYRRVPCVKKGGIRFTINGHSYENLVLVTNV----AGPGD 158
 EMBL; M97880; -; NOT_ANNOTATED_CDS. HSSP; P02965; 1CIY.
 the European Bioinformatics Institute. There are no restrictions
 -!- SIMILARITY: BELONGS TO THE DELTA ENDOTOXIN FAMILY.
 SEQUENCE
 Pfam; PF00555; endotoxin;
 InterPro; IPR001178; Endotoxin.
 365 SNPTFRPLQQPWPAPPFNLRGVEGVEFSTPLNSFTYRGRGTVDSLTELPPEDNS--VPPR 422
 310 FTDWFSVGRNFYWGGHRVISNRIGG----GNITSPIYGREANQEPPRSFTFN-GPVFRTL 36.
100 PHFD--MAEPAFLQIGVYRAG-----
 57
 Local
 2 YSSWQSAHATFYGGGD--ASGTMGGTCGYGNLYSTGY---TNTAALSTVLFNDGAACRSC 56
 EPITHELIAL CELLS OF INSECTS. TOXIC TO SPODOPTERA EXIGUA AND TRICHPLUSIA NI.
DEVELOPMENTAL STAGE: THE CRYSTAL PROTEIN IS PRODUCED DURING
 MISCELLANEOUS: TOXIC SEGMENT OF THE PROTEIN IS LOCATED IN THE
 OF THE SPORE COAT
 SPORULATION AND IS ACCUMULATED BOTH AS AN INCLUSION AND AS
 N-TERMINUS
 Sporulation.
 Similarity
 1176 AA; 132867 MW; 108233494C2AC018 CRC64;
 Conservative
 STANDARD;
 -YELRCDNDGQWCLP-GSVTVTATNLCPPNYALPNDDGGWCNPPR 99
 6.7%; Score 84.5;
22.5%; Pred. No. 1
 30;
 PRT;
 Mismatches
 No. 12;
 1176 AA
 DB 1; Length 1176;
 98;
 --IVPVSYRRVPCVK---- 131
 Indels
 99;
 PART
 Gaps
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| Search completed: October 11, 2002, 14:57:35<br>Job time : 7.83764 secs | Db 539 GSTTGNQGFPSTMSANGALTSQSFRFAEFPVGISASGSQGASISISNNV 587 | QY 166 GSSTGWQPMSRNWGQNWQSNSYLDGQSLSFQVAVSDGRTVT-SNNV 210 | Db 479 TSGTSVVRGPGFTGGDITRTNVNGSVLSMSLNFSNTTLQRYRVRVRVRAASQTMVMSVTVG 538 | Oy 132KGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIK 165 | ASSIFE LITHER PERSON LITTER PROBLEM 478 |
|-------------------------------------------------------------------------|--------------------------------------------------------------|-----------------------------------------------------------|--------------------------------------------------------------------------|----------------------------------------------|-----------------------------------------|
|                                                                         | :     :::     <br>ISASGSQGASISISNNV 587                      | -QVAVSDGRTVT-SNNV 210                                     | TLQRYRVRVRYAASQTMVMSVTVG 538                                             | VLVTNVAGPGDVQSVSIK 16                        | SATURNITYPDVINQIPLVKAFNL 471            |



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 Minimum DB seq length: Maximum DB seq length:
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 Run on:
 OM protein - protein search, using sw model
 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Listing first 45 summaries
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Sequence 6, Appli
 Description
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| Query Match Best Local Similarity 100.0%; Best Local Similarity 100.0%; Matches 226; Conservative Qy 1 DYSSWQSAHATFYGGGDASGTWG                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | RESULT 1 US-08-440-517A-6 : Sequence 6, Application US/08440: : Sequence 6, Application US/08440: : Patent No. 5959082 : GENERAL INFORMATION: APPLICANT: COSGROVE, DANIEL: APPLICANT: SUIL/JUN ITTILE OF INVENTION: PURIFIED NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS: ADDRESSEE: PENNSYLVANIA STREET: 113 TECHNOLOGY CENT CITY: UNIVERSITY PARK STATE: PENNSYLVANIA COUNTRY: UNIVERSITY PARK STATE: PENNSYLVANIA COUNTRY: UNITED STATES OF A COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK COMPUTER: WOLDERFECT 5.1 CURRENT APPLICATION NUMBER: US/08/4 FILING DATE: APPLICATION UMBER: US/08/4 FILING DATE: CLASSIFICATION: 530 INFORMATION FOR SED ID NO: 6: SEQUENCE CHARACTERISTICS: LENGTH: 226 TYPE: AMNO ACID TOPOLOGY: UNKNOWN | 28 202 16.1 245 4 29 169 13.4 200 4 30 168 13.4 197 4 31 125.5 10.0 145 4 32 109.5 8.7 145 4 34 109.5 8.7 145 4 35 109.5 8.7 145 4 36 107.5 8.6 145 4 37 106.5 8.6 145 4 38 102 8.1 138 4 40 89 7.1 1147 1 40 89 7.1 1165 2 41 87 6.9 759 5 |
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US-09-092-160-6
 ; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis; OTHER INFORMATION: expansin US-09-092-160-6
 B
 Qy
 Дb
 QΥ
 ф
 Qy
 US-09-092-160-7
 GENERAL INFORMATION:
 Sequence 6, Application US/09092160C Patent No. 6255466
 GENERAL INFORMATION:
APPLICANT: COSGTOVE, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
 SEQ ID NO 6
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 Sequence 7, Application US/09092160C Patent No. 6255466
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 EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/
EARLIER FILING DATE: 1994-05-12
 FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
 APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
 EARLIER APPLICATION NUMBER: 08/060,944 EARLIER FILING DATE: 1993-05-12
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EARLIER FILING DATE: 1995-05-12
 APPLICANT: Guiltinan, Mark J
 NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn Ver. 2.1
 APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 APPLICANT: Shcherban, Tatyana
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS FILE REFERENCE: 1194/IC114US3 CURRENT APPLICATION NUMBER: US/09/092,160C CURRENT FILLING DATE: 1998-05-05 EARLIER APPLICATION NUMBER: 08/440,517
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 08/242,090
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 Gaps
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 US-08-440-517A-2
 US-08-440-517A-2
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 Matches 177;
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EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
 SOFTWARE: PatentIn Ver. 2.1
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 LENGTH: 227
TYPE: PRT
ORGANISM: Artificial Sequence
 OTHER INFORMATION: Description of Artificial Sequence: cucumber OTHER INFORMATION: expansin
 FEATURE:
 CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
 COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
 CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE,
ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
 CURRENT APPLICATION DATA:
 APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 SEQUENCE CHARACTERISTICS:
 NUMBER OF SEQUENCES:
 APPLICANT:
 APPLICANT:
 APPLICANT:
 180 QNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
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 STREET: 113 TECHNOLOGY CENTER CITY: UNIVERSITY PARK
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 1 DYSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTYLFNDGAACRSCYEL 59
 FILING DATE:
 COMPUTER:
 TYPE:
 APPLICATION NUMBER:
 SOFTWARE:
 OPERATING SYSTEM:
 COUNTRY:
 TOPOLOGY:
 LENGTH:
 227
 Similarity
 16802-7000
 AMINO ACID
 PENNSYLVANIA
 Conservative
 UNITED STATES OF AMERICA
 SHCHERBAN, TATYANA;
 GUILTINAN,
 COSGROVE, DANIEL J.;
 WORDPERFECT 5.1
 UNKNOWN
 NEC
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 US/08/440,517A
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 2
 21; Mismatches
 DB 4; Length 227;
 28; Indels
Length 228;
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 Gaps
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Ξ.

Query Match

76.3%;

Score 959.5;

ВG

2;

Matches

Best Local Similarity

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APPLICANT: COSGROVE, Daniel J
APPLICANT: MCQUeen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Schebtban, Tatyana
APPLICANT: Shchetban, Tatyana
APPLICANT: Shchetban, Tatyana
APPLICANT: Shchetban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 11947/10114US3
CURRENT APPLICATION NUMBER: U5/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1993-05-12
EARLIER FILING DATE: 1993-05-12
EARLIER FILING DATE: 1993-05-12
EARLIER FILING DATE: 1993-05-12
 ; OTHER INFORMATION: Xaa is unknown or other US\hbox{-}09\hbox{-}092\hbox{-}160\hbox{-}2
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 Query Match
 SEQ ID NO 2
 Sequence 2, Application US/09092160C Patent No. 6255466
 GENERAL INFORMATION:
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 SOFTWARE: PatentIn Ver. 2.1
 NUMBER OF SEQ ID NOS:
 LENGTH: 228
TYPE: PRT
ORGANISM: Artificial Sequence
 NAME/KEY: UNSURE LOCATION: 211
 OTHER INFORMATION: Description of Artificial Sequence: rice expansin
 FEATURE
 FEATURE
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 Conservative
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 23; Mismatches
 1.2e-83;
 DB 4; Length 228;
 31; Indels
 Indels
 1; Gaps
 Gaps
 1;
APPLICANT: COSGROVE, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shcherban, Tatyana
APPLICANT: Shcherban, Tatyana
APPLICANT: Sh. Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
 US-09-092-160-5
 RESULT 7
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 В
 US-08-440-517A-5
 ; Patent No. ; GENERAL II
 US-08-440-517A-5
 RESULT 6
 GENERAL INFORMATION:
 Sequence 5, Application US/09092160C Patent No. 6255466
 Matches
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 Sequence 5,
 CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
 GENERAL INFORMATION:
 SEQUENCE CHARACTERISTICS:
 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
 COMPUTER READABLE FORM:
 179 GONWOSNSYLDGOSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
 NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
 178 GQNWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
 118 VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW 177
 TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
 APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
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OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
 STREET: 113 TECHNOLOGY CENTER CITY: UNIVERSITY PARK
 1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFEL 60
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 TOPOLOGY:
 LENGTH:
 FILING DATE:
 MEDIUM TYPE:
 COUNTRY:
 ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
 1 DYSSWQSAHATEYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLENDGAACRSCYEL 59
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 158;
 Similarity
 16802-7000
 AMINO ACID
 , Application US/08440517A
5959082
 PENNSYLVANIA
 Conservative
 UNITED STATES OF AMERICA
 SHI, JUN
 UNKNOWN
 SHCHERBAN, TATYANA;
 FLOPPY DISK
 68.7%; Score 863.5; DB 2; Length 225; 69.3%; Pred. No. 1.5e-74;
 US/08/440,517A
 24; Mismatches
 41; Indels
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 US-09-092-160-5
 US-08-845-539-2
 Matches 158; Conservative
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 SEQ ID NO 5
 EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER TILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
 Sequence 2, Application US/08845539 Patent No. 5929303
 GENERAL INFORMATION:
 OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis OTHER INFORMATION: expansin
 ORGANISM: Artificial Sequence
 TYPE: PRT
 FEATURE:
 TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO:
 ENGTH: 225
 TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
 SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM:
 CORRESPONDENCE ADDRESS:
 APPLICANT:
 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
 NUMBER OF SEQUENCES:
 178
 118 VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW 177
 SEQUENCE CHARACTERISTICS:
 ATTORNEY/AGENT INFORMATION:
 179 GQNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
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 61 TCEDDPEWCIPGSI-IVRYNLA--NFALANDNGGWCNPPLKHFDLAEFAFLQIAQYRAGI 117
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 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
 STREET: Two ______
CITY: San Francisco
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 ZIP:
 NAME: Bastian, Kevin REGISTRATION NUMBER:
 CLASSIFICATION:
 COUNTRY:
 ADDRESSEE:
 REFERENCE/DOCKET NUMBER:
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 94111-3834
 E: Townsend and Townsend and Crew LLP Two Embarcadero Center, Eighth Floor
 Bennett, Alan B.
Rose, Jocelyn K.C.
225 amino acids
 USA
 25-APR-1997
 68.7%; Score 863.5; DB 4 69.3%; Pred. No. 1.5e-74; ative 24; Mismatches 41
 US/08/845,539
 34,774
 023070-078200US
 DB 4; Length
 41;
 Indels
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 ; MOLECULE TYPE: protein US-08-845-539-2
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 US-08-440-517A-3
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 US-08-440-517A-3
 Sequence 3, Applic
Patent No. 5959082
 Matches 138; Conservative
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 Best Local Similarity
 Matches 146;
 Query Match
 GENERAL INFORMATION:
APPLICANT: COSGROVE, DANIEL J.;
 CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
 NUMBER OF SEQUENCES: 6
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MEDIUM TYPE: FLOPPY DISK
 CORRESPONDENCE ADDRESS:
 APPLICANT:
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 STREET: 113 TECHNOLOGY
CITY: UNIVERSITY PARK
 ADDRESSEE:
 APPLICATION NUMBER: FILING DATE:
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 OPERATING SYSTEM:
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 COUNTRY:
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 16802-7000
 Application US/08440517A
 PENNSYLVANIA
 113 TECHNOLOGY CENTER
 GUILTINAN,
 UNITED STATES OF AMERICA
 SHCHERBAN, TATYANA;
 Conservative
 WORDPERFECT 5.1
 NEC 286
 INTELLECTUAL PROPERTY OFFICE, PENNSYLVANIA STATE UNIVERSITY
 UNKNOWN
 63.0%;
71.1%;
 62.6%; Score 787; DB 2; 65.2%; Pred. No. 2.8e-67;
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b; Pred. No. 1.1e-67;
24; Mismatches 27;
 21; Mismatches
 DB 2; Length 222;
 47;
 Length 225;
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 Indels 10;
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GENERAL INFORMATION:
APPLICANT: COSGTOVE, Daniel J
APPLICANT: GOSGTOVE, Daniel J
APPLICANT: GUILtinan, Mark J
APPLICANT: Guiltinan, Mark J
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/04/0.517
EARLIER APPLICATION NUMBER: 08/440.517
EARLIER APPLICATION NUMBER: 08/42,090
EARLIER APPLICATION NUMBER: 08/05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
EARLIER FILING DATE: 1993-05-12
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EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
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 US-09-092-160-3
 GENERAL INFORMATION:
 Sequence 2, Application US/09362642 Patent No. 6350935
 APPLICANT:
APPLICANT:
APPLICANT:
 Matches
 Query Match
 SEQ ID NO 3
 paceurence 3, Application US/09092160C Patent No. 6255466
 TITLE OF INVENTION:
 NAME/KEY: UNSURE
LOCATION: (14)..(58)
OTHER INFORMATION: Xaa is unknown or other.
 LENGTH: 222
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 FEATURE: OTHER INFORMATION: Description of Artificial Sequence: rice expansin FEATURE:
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 183 QSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
 177 QSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 220
 183 OSNSYLDGOSLSFOVAVSDGRTVTSNNVVPAGWOFGQTFEGGQF 226
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 146;
 Rose, Jocelyn K.C.
The Regents of the University of California
VENTION: Fruit-Specific and Ripening Regula
 Bennett, Alan B.
 Conservative
 62.6%;
 21;
 Score 787; DB 4; Length 222; Pred. No. 2.8e-67;
 Mismatches
Ripening
 47; Indels
Regulation Expansin Genes
 Gaps
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US-08-440-517A-4
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 В
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Query Match 59.0
Best Local Similarity 64.0
Matches 137; Conservative
 SOFTWARE: Pa
SEQ ID NO 2
LENGTH: 225
 Sequence 4, Patent No.
 Matches 137;
 Query Match
 GENERAL INFORMATION:
 INFORMATION FOR SEQ ID NO:
 CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
 TITLE OF INVENTION: to Control Fruit Texture and Softening FILE REFERENCE: 023070-07821005
 NUMBER OF SEQ ID NOS:
 OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
 NUMBER OF ENVENTION: PURIFIED EXPANSIN PROT.
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE,
ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
 SEQUENCE CHARACTERISTICS:
 COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK
 APPLICANT:
 APPLICANT:
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 212 GONWQSNAVLTGQS 225
 179 GONWOSNSYLDGOS 192
 TYPE:
 FILING DATE:
 STREET: 113 TECHNOLOGY CITY: UNIVERSITY PARK
 CLASSIFICATION: 530
 COMPUTER:
 92 NTPNWKWCLPGNPSILITATNFCPPNYALPNDNGGWCNPPRPHFDLAMPMFLKLAQYRAG
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 32 SWETAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGLSCGACFELKCT 91
 Local Similarity
 4 SWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTYLENDGAACRSCYELRCD 62
 16802-7000
 AMINO ACID
 , Application US/08440517A 5959082
 PatentIn Ver. 2.1
 PENNSYLVANIA
 113 TECHNOLOGY CENTER
 COSGROVE, DANIEL J.;
 UNITED STATES OF AMERICA
 GUILTINAN,
 UNKNOWN
 NEC 286
 SHCHERBAN, TATYANA;
 Conservative
 JUN
 62.3%;
59.0%; Score 742; DB 2; 64.0%; Pred. No. 5.4e-63; tive 24; Mismatches 49
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 US/08/440,517A
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 24; Mismatches
 Score 783.5; DB 4; Pred. No. 6.1e-67;
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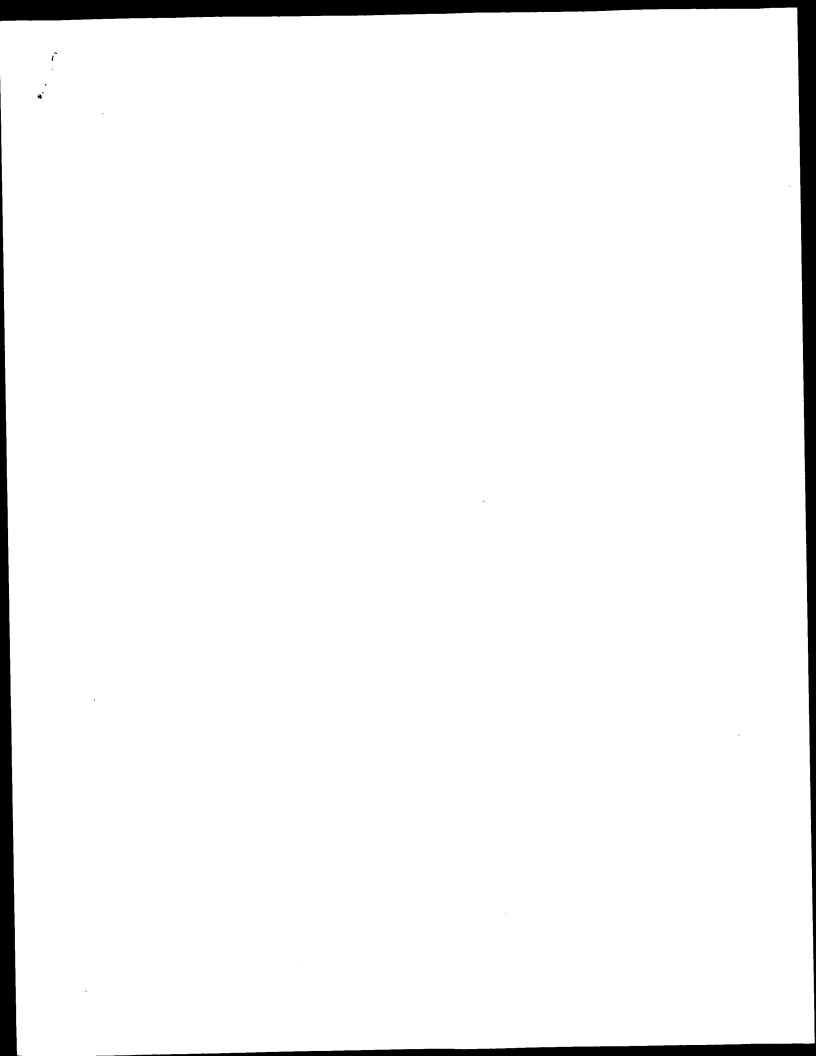
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6 QSAHATEYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTYLENDGAACRSCYELRCD+N 63

<u>ب</u>

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APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: McQueen-Mason, Simon
APPLICANT: Shcherban, Tatyana
APPLICANT: Shcherban, Tatyana
APPLICANT: Shcherban, Tatyana
APPLICANT: Shcherban, Tatyana
APPLICANT: Shcherban, Tatyana
APPLICANTO: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER APPLICATION NUMBER: 08/242,090
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EARLIER APPLICATION NUMBER: 08/260,944
EARLIER FILING DATE: 1993-05-12
RUMBER OF SEQ ID NOS: 7
NUMBER: Date 1515
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 ; OTHER INFORMATION: US-09-092-160-4
 RESULT 13
US-09-092-160-4
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RESULT 14
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 Sequence 4, Application US/09092160C Patent No. 6255466
 GENERAL INFORMATION:
 SEQ ID NO 4
 Matches
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Best Local Similarity
 SOFTWARE: PatentIn Ver. 2.1
 OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis OTHER INFORMATION: expansin
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 ORGANISM: Artificial Sequence
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 Mismatches
 DB 4; Length 227;
 49; Indels
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 US-08-845-539-6
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CURRENT APPLICATION NUMBER: US/9/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
 Patent No.
 Sequence 6,
 GENERAL INFORMATION:
 Sequence 6, Application US/09362642 Patent No. 6350935
 Matches 128;
 Query Match
 GENERAL INFORMATION:
APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
 APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 033070-778210US
 TELEFAX: (415) 576-03: INFORMATION FOR SEQ ID NO:
 SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
 TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
 TELECOMMUNICATION INFORMATION:
 ATTORNEY/AGENT INFORMATION:
 CORRESPONDENCE ADDRESS:
 NUMBER OF SEQUENCES:
 MOLECULE TYPE:
 SEQUENCE CHARACTERISTICS:
 127 VPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQNWQ 183
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123 VPCRKQGGIRFTINGFRYFNLVLIINVAGAGDIVRVSVKGSNTGWMSMSRNWGQNWQ 179
 NAME: Bastian, Kevin L. REGISTRATION NUMBER: 34,774 REFERENCE/DOCKET NUMBER: 02
 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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 TOPOLOGY:
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 San Francisco
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 California
 Two Embarcadero Center, Eighth Floor
 179 amino acids
 (415) 576-0200
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 57.8%; Score 726.5; 72.3%; Pred. No. 1.2
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Maximum Match 100%
Listing first 45 summaries
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 Database
 Total number of hits satisfying chosen parameters:
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 Scoring table:
 Sequence:
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Perfect score:
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 Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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1011.5
960.5
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20: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
21: /SIDSI/gcgdata/geneseq/geneseq-embl/AA1990.DAT:*
22: /SIDSI/gcgdata/geneseq/geneseqp-embl/AA1990.DAT:*
 GenCore version 5.1.3 Copyright (c) 1993 - 2002 Compugen Ltd
 Length DB
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 IJ
 AAG51647
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AAG06545
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 AAR94532
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 SUMMARIES
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Cucumber expansin-
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 Description
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| <b>4</b><br>U | 4 4      | 43       | 42      | 41       | 40      | 39       | 38       | 37       | 36       | 35            | 34           | 33       | 32       | 31       | 30       | 29       | 28       | 27       | 26       | 25       | 24       | 23       | 22       | 21       | 20                 | 19       | 18       | 17       | 16       | 15       | 14       | 13              | 12                |
|---------------|----------|----------|---------|----------|---------|----------|----------|----------|----------|---------------|--------------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|----------|--------------------|----------|----------|----------|----------|----------|----------|-----------------|-------------------|
| 8 L 5 . 5     | 2 8 1 6  | 816      | 816     | 816      | 863.5   |          | 864      | $\sim$   | 864.5    | 871           |              | 880.5    |          | 895      | 895      | 895      | 899.5    | LO.      | 900      | 900      | . 1.3    | 1.)      | N 1      | m        | $\sim$             | $\sim$   | m        | $\sim$   | $\sim$   | 938.5    | 948      | 948             | 959.5             |
|               |          |          | -       |          |         |          |          |          |          |               |              |          |          |          |          | _        | -        | :        |          |          |          | -        |          |          |                    | 4        | 4        | 4        | •        | 4        | 75.4     | 5               | 6                 |
| 210           | 255      | 255      | 221     | 221      | 225     | 207      | 207      | 257      | 255      | 257           | 280          | 258      | 250      | 255      | 249      | 242      | 257      | 255      | 249      | 241      | 273      | 262      | 250      | 282      | 281                | 263      | 253      | 253      | 251      | 251      | 253      | 253             | 228               |
| 21            | 21       | 21       | 21      | 21       | 17      | 21       | 21       | 21       | 21       | 22            | 21           | 21       | 21       | 21       | 21       | 21       | 21       | 21       | 21       | 21       | 21       | 21       | 22       | 21       | 21                 | 22       | 21       | 21       | 21       | 21       | 21       | 21              | 17                |
|               | AAG51012 | AAG15693 |         | AAG15694 |         | AAG46484 | AAG25444 | AAG30324 | AAG30325 | AAE00413      | AAG09620     | AAG09621 | AAG09622 | AAG36568 | AAG36569 | AAG36570 | AAG36445 | AAG05451 | AAG05452 | AAG05453 | AAG29930 | AAG29931 | AAE00414 | AAG23850 | AAG43341           | AAE00412 | AAG43342 | AAG23851 | AAG43343 | AAG23852 | AAG46483 | AAG25443        | AAR94528          |
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## ALIGNMENTS

RESULT 1 AAR94532

AAR94532 standard; Protein; 227

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Disclosure; Page 32-33; 60pp; English.
 Expansin proteins which alter the mechanical strength of poly:saccharide(s) - useful in paper \mathsf{mfr.} and \mathsf{recycling}
 Cosgrove DJ,
 (PENN-) PENN STATE RES FOUND.
 12-MAY-1995;
12-MAY-1993;
 WPI; 1996-201150/21.
 12-MAY-1994;
 04-APR-1996
 AU9540262-A
 Arabidopsis sp.
 polysaccharide
 McQueen-Mason S;
 95US-0440517.
93US-0060944.
 94AU-0068320
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Expansin; plant cell wall; cellulose; paper recycling; de-inking;

Arabidopsis expansin.

08-JUL-1996 AAR94532;

(first entry)

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Best Local
 Expansins are a novel class of proteins that catalyse the extension of plant cell walls and the weakening of the hydrogen bonds in pure cellulose. 2 Expansins (AAR94528 and AAR94529) have been identified rice and 3 in Arabidopsis (AAR94530-32). A cDNA clone (AAT13320) coding for cucumber expansin 29 (AAR94527) has been obtd. Expansins can be used e.g. in the mfr., de-inking and recycling of paper, in the textile industry, to aid delignification processes, to alter gel mechanical strength, etc.
 Sequence
 Cucumber expansin-29.
 AAR94527 standard; Protein; 227
 WPI;
 12-MAY-1995;
12-MAY-1993;
 04-APR-1996
 Cucumis sativus
 polysaccharide;
 Expansin-29;
 08-JUL-1996
 Cucumber expansin-29 (AAR94527) is a member of a novel class of proteins that catalyse the extension of plant cell walls and the weakening of the hydrogen bonds in pure cellulose. It can be obt by expression of an isolated cDNA clone (see AAT13320) in bacteri
 Expansin proteins which alter the mechanical strength of
poly:saccharide(s) - useful in paper mfr. and recycling
 Cosgrove DJ,
 (PENN-) PENN
 AU9540262-A
уd
 Claim 7; Page 30; 60pp; English
 poly:saccharide(s)
 12-MAY-1994;
 181
 181
 121
 121
 61
 61
expression
 CDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHEDMAEPAFLQIGVYRAGIV 120
 DYSSWOSAHATFYGGGDASGTMGGTCGYGNLYSTGYTNTAALSTVLFNDGAACRSCYELR 60
 PVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQ 180
 PVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVÅGPGDVQSVSIKGSSTGWQPMSRNWGQ
 CDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGIV
 DYSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGYTNTAALSTVLFNDGAACRSCYELR
 1996-201150/21.
DB; AAT13320.
 NWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFE-GGQF 226
 Similarity
 227 AA;
 Conservative
 plant cell wall; cellulose; paper recycling; de-inking;
 (first entry)
 STATE RES FOUND
 93US-0060944
 95US-0440517.
 94AU-0068320
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 cucumber.
 99.2%;
99.6%;
 Burpee Pickler
 useful in paper mfr.
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 Score 1246.5; DB 17; Length Pred. No. 4.4e-113;
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 other host cells. Expansin proteins have also been identified in oat coleoptiles, in Arabidopsis (see AAR94530-32) and in rice (AAR94528-29), and appear to be broadly distributed throughout the plant kingdom. Expansins can be used e.g. in the mfr., de-inking and recycling of paper, in the textile industry, to aid delignification processes, to alter gel mechanical strength, etc.
16-APR-1999
119-APR-1999
21-APR-1999
23-APR-1999
23-APR-1999
30-APR-1999
30-APR-1999
30-APR-1999
04-MAY-1999
06-MAY-1999
 25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
 06-APR-1
 Sequence
 Arabidopsis thaliana protein fragment SEQ ID
 AAG06546 standard; Protein;
 Arabidopsis thaliana
 Protein identification; signal transduction pathway; metabolic pathway;
 17-OCT-2000
 AAG06546;
 06-SEP-2000
 EP1033405-A2
 hybridisation assay;
 25-FEB-2000;
 181
 180 QNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF
 121
 120
 61 TCTNDPKWCLPGTIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGI 120
 60
 Local
 1 DYSSWQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYEL
 DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM
 RCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGI 119
 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG
 VPVSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWG
 Similarity
 227 AA;
 Conservative
 (first entry)
 2000EP-0301439
 99US-0127462.

99US-0128714.

99US-012845.

99US-0130077.

99US-0130610.

99US-0130610.

99US-0130610.

99US-013149.

99US-0132048.

99US-0132484.

99US-0132484.

99US-0132486.

99US-0132487.
 99US-0123180
99US-0123548
 99US-0126785
 80.5%;
77.1%;
 genetic mapping; gene expression control;
 23;
 Score 1011.5;
Pred. No. 3.1
 Mismatches
 5; DB 17;
1.1e-90;
 NO: 3357
 28; Indels
 Length 227;
 226
 1.
 Gaps
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 179
 60
 59
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 Arabidopsis thaliana.
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 06-SEP-2000
 EP1033405-A2
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|------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------|-------------------------------------------------------------------------|------------------------------------------------|-------------------------------------------------------------------------|------------------------------------------------|-----------------------|------------------------------------------------|-------------------------------------------------------------------------|-----------------------|-----------------------|------------------------------------------------|------------------------------------------------|-----------------------|-----------------------|------------------------------------------------|------------------------------------------------|-----------------------|------------------------------------------------|-----------------------|-----------------------|------------------------------------------------|-----------------------|-----------------------|------------------------------------------------|-----------------------|--------------------------------------|----------------------|----------------------|--------------------------------------|-----------------------|-----------------------|----------------------|----------------------|------------------------------|----------------------|----------------------|
|                                                                                                      |                                                                            | ~ ~ ~                                                                   | ਲੱਲੋਂ :                                        | ק קים<br>א קים                                                          | PR                                             | P Z                   | ק<br>ק                                         | PR                                                                      | PR                    | g g                   | д<br>ж                                         | PR<br>PR                                       | PR                    | PR                    | PR                                             | PR R                                           | PR<br>R               | PR<br>R                                        | PR                    | PR :                  | PR                                             | PR                    | PR                    | P R                                            | PR                    | PR                                   | בר<br>ג              | PR                   | Q Q                                  | קק<br>קק              | ט<br>ע ע              | PR                   | ק<br>א               | g g                          | PR                   | PR:                  |
| 08-<br>09-<br>12-                                                                                    | 01-                                                                        | 30-<br>30-                                                              | 23-                                            | 22-                                                                     | 18-                                            | 18-                   | 18.                                            | 18-                                                                     | 18-                   | 180                   | 17.                                            | 16.5                                           | 14.                   | 10.                   | 074                                            | 00.01                                          | 28                    | 25                                             | 210                   | 19                    | 14                                             | 14                    | 14                    | 107                                            | 06                    | 0.5                                  | 0 6                  | 30                   | ນ ຄຸນ<br>ສີ ພ                        | 23                    | ر<br>19               | 16                   | 000                  | 20                           | 225                  | N<br>W               |
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|                                                                                                      |                                                                            |                                                                         | ** ** *.                                       |                                                                         | •• ••                                          | ٠. ٠.                 | ٠. ٠.                                          | •• ••                                                                   | ٠. ٠.                 | •••                   |                                                |                                                |                       |                       |                                                |                                                |                       |                                                |                       |                       |                                                |                       |                       |                                                |                       |                                      |                      | ъ.                   |                                      |                       |                       |                      | :                    | 9 9                          | 9 9                  | 9 .                  |
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| 144                                                                                                  | 144                                                                        | 144                                                                     | 014                                            | 133                                                                     | 013<br>013                                     | 013                   | 013                                            | 013                                                                     | 013                   | 013                   | 013                                            | 013                                            | 013                   | 013                   | 013                                            | 013                                            | 510                   | 013                                            | 213                   | 01                    | 201                                            | 010                   | 011                   | 22                                             | 01                    | 22.                                  | 20                   | 200                  | 22                                   | 25                    | 20                    | 01                   | 20                   | 200                          | 25                   | င္ခ်င္               |
| 12390.<br>12803.<br>12920.<br>12977.<br>13542.                                                       | 154<br>055                                                                 | )823.<br>)991.                                                          | )354<br>)695.                                  | 9817.                                                                   | 9750.<br>9763.                                 | 9462.                 | 9460.                                          | 9458.                                                                   | 9456                  | 9455                  | 9492                                           | 9452                                           | 8847<br>9119          | 8094<br>8540          | 7502                                           | 7222                                           | 6392<br>6782          | 5629<br>6021                                   | 5124<br>5353          | 4941                  | 4370                                           | 4219<br>4221          | 4218                  | 2863                                           | 2485                  | 2485                                 | 2407                 | 2048                 | 0891                                 | 0510                  | 0077                  | 9845                 | 28234                | 27462                        | 26264                | 25788                |
|                                                                                                      |                                                                            |                                                                         |                                                |                                                                         |                                                |                       | •                                              | • •                                                                     | • •                   | • •                   |                                                | • •                                            | •                     | • •                   | • • •                                          | •                                              | •                     | • •                                            |                       |                       | • •                                            |                       | • •                   | •                                              | •                     |                                      | •                    |                      | :                                    |                       | •                     |                      | •                    | : :                          | ·· <del>·</del>      |                      |
|                                                                                                      |                                                                            |                                                                         |                                                |                                                                         |                                                |                       |                                                |                                                                         |                       |                       |                                                |                                                |                       |                       |                                                |                                                |                       |                                                |                       |                       |                                                |                       |                       |                                                |                       |                                      |                      |                      |                                      |                       |                       |                      |                      |                              |                      |                      |
|                                                                                                      |                                                                            |                                                                         |                                                |                                                                         |                                                |                       |                                                |                                                                         |                       |                       |                                                |                                                |                       |                       |                                                |                                                |                       |                                                |                       |                       |                                                |                       |                       |                                                |                       |                                      |                      |                      |                                      |                       |                       |                      |                      |                              |                      |                      |
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|                                                                                                      |                                                                            |                                                                         |                                                |                                                                         |                                                |                       |                                                |                                                                         |                       |                       |                                                |                                                |                       |                       |                                                |                                                |                       |                                                |                       |                       |                                                |                       |                       |                                                |                       |                                      |                      |                      |                                      |                       |                       |                      |                      |                              |                      |                      |
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|                                                                                                      |                                                                            |                                                                         |                                                |                                                                         |                                                |                       |                                                |                                                                         |                       |                       |                                                |                                                |                       |                       |                                                |                                                |                       |                                                |                       |                       |                                                |                       |                       |                                                |                       |                                      |                      |                      |                                      |                       |                       |                      |                      |                              |                      |                      |
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|                                                                                                      |                                                                            |                                                                         |                                                |                                                                         |                                                |                       |                                                |                                                                         |                       |                       |                                                |                                                |                       |                       |                                                |                                                |                       |                                                |                       |                       |                                                |                       |                       |                                                |                       |                                      |                      |                      |                                      |                       | _                     |                      |                      |                              |                      |                      |
|                                                                                                      |                                                                            |                                                                         |                                                |                                                                         |                                                |                       |                                                | <u>.                                    </u>                            |                       |                       |                                                |                                                |                       |                       |                                                |                                                |                       |                                                |                       |                       |                                                |                       | -                     |                                                |                       |                                      |                      |                      |                                      |                       |                       |                      | -                    |                              |                      |                      |
| ר א<br>ק<br>ק<br>ק<br>ק<br>ק<br>ק                                                                    | PR<br>PR<br>PR                                                             | ק<br>אם<br>אם                                                           | PR<br>PR                                       | אין<br>קק                                                               | PR                                             | ליק<br>אינ            | אין<br>אק                                      | יינ<br>קר                                                               | PR                    | PR                    | PR<br>PR                                       | PR                                             | אַקי                  | מק                    | אק<br>אק                                       | PR                                             | אין<br>אין            | קטי<br>געי                                     | PR                    | PR                    | PR                                             | PR PR                 | PR                    | PR                                             | PR                    | PR                                   | PR                   | PR                   | אק                                   | PR                    | PR                    | PR                   | PR                   | PR<br>PR                     | יע                   | PR                   |
| 2843                                                                                                 | 20-                                                                        | 10-                                                                     | 202                                            | 30,27                                                                   | 276                                            | 25.5                  | 222                                            | 220                                                                     | 18                    | 16<br>17              | 13                                             | 11                                             | 10                    | 090                   | 005                                            | 054                                            | 04 0                  | 200                                            | 202                   | 27                    | 27                                             | 26                    | ນຸນ                   | 2 2                                            | 100                   | N N                                  | 22                   | 201                  | 200                                  | 2 2 !                 | 11.                   | 1.5                  | 1.5                  |                              | 11                   | <u> </u>             |
| 23 - SEP<br>24 - SEP<br>28 - SEP<br>29 - SEP                                                         | 15-SEP<br>16-SEP<br>20-SEP                                                 | 10-SEP<br>13-SEP                                                        | 31-AUG                                         | 27 - AUG                                                                | 26 - AUG                                       | 25-AUC                | 23-AUC                                         | 20-AUC                                                                  | 18-AUC                | 16-AUG                | 13-AU0                                         | 11-AU0                                         | 10-AU                 | 09-AU                 | 05-AU                                          | 04 - AU                                        | 04-AU                 | 02-AU                                          | 02-AU                 | 27 - JU               | 27 - JU<br>27 - JU                             | 26-JU                 | 23-JU                 | 22-JU<br>23-JU                                 | 22-JU                 | 22-JU<br>22-JU                       | 21-JU                | 21 - JU              | 20-JU                                | 20-10                 | 19-JU                 | 19-JU                | 19-50                | 19-JU                        | 11                   | 15-JUL               |
| 23-SEP-199<br>23-SEP-199<br>24-SEP-199<br>28-SEP-199<br>29-SEP-199                                   | 15-SEP-19                                                                  | 07-SEP-19<br>10-SEP-19<br>13-SEP-19                                     | 31-AUG-19<br>01-SEP-19                         | 27-AUG-19<br>27-AUG-19                                                  | 26-AUG-19<br>27-AUG-19                         | 25-AUG-19             | 23-AUG-19                                      | 20-AUG-19                                                               | 18-AUG-19             | 16-AUG-19             | 13-AUG-19<br>13-AUG-19                         | 11-AUG-19<br>12-AUG-19                         | 10-AUG-19             | 09-AUG-19             | 05-AUG-19<br>06-AUG-19                         | 04-AUG-19                                      | 04-AUG-19             | 02-AUG-19                                      | 02-AUG-19             | 27 - JUL - 19         | 27-JUL-19<br>27-JUL-19                         | 26-JUL-19             | 23-JUL-19             | 22-JUL-19<br>23-JUL-19                         | 22-JUL-19             | 22-JUL-19                            | 21-JUL-19            | 21 - JUL - 19        | 20-JUL-19                            | 20-JUL-1              | 19-JUL-1              | 19-JUL-1             | 19-JUL-1             | 19-JUL-1                     | 16-JUL-1             | 15-JUL-1             |
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 AAG51645 standard;
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Local Similarity
les 168; Conser
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                                                                                                SNSYLDGOSLSFQVAVSDGRTVTSNNVVPAGWOFGQTFEGGQF
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Protein; 280
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75.3%;
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                                                                                                                                                                            WQSAHATFYGGGDASGTWGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYELRCDN 63
                         SNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
                                                                    YRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQNWQ
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                                                                                                           DGKWCLPGSIVVTATNFCPPNNALANNNGGWCNPPLEHFDLAQPVFQRIAQYRAGIVPVS
                                                      YRRVPCRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAAIKGSRTVWQAMSRNWGQNWQ
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168; Conserv
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3-0155659.
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75.3%;
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Pred. No. 3.7e-85;
'2; Mismatches 32;
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Best Local
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                                                                                                                                                                                                                                                                                  Expansins are a novel class of proteins that catalyse the extension of plant cell walls and the weakening of the hydrogen bonds in pure cellulose. 2 Expansins (AAR94528 and AAR94529) have been identified rice and 3 in Arabidopsis (AAR94530-32). A cDNA clone (AAT13320) coding for cucumber expansins 29 (AAR94527) has been obtd. Expansins can be used e.g. in the mfr., de-inking and recycling of paper, in the textile industry, to aid delignification processes, to alter gel mechanical strength, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                Expansin proteins which alter the mechanical strength poly:saccharide(s) - useful in paper mfr. and recycli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1996-201150/21.
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12-MAY-1993;
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                                                                                                                                                                     WQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYELRCDN 63
                                                                                                   DGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVPVA 124
                                                                                                                  DGOWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGIVPVS 123
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                       SNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEG
                                                  YRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQNWQ
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3; Mismatches 31
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990S-0141287

990S-014287

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990S-014332

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PR 11 -MC -1999 99US-0148171
PR 13 -MC -1999 99US-0148564
PR 15 -MC -1999 99US-0148564
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Search completed: October 11, 2002, 14:56:44 Job time: 26.0184 secs

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Result
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Perfect score:
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      1265
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1: sp_archea:*

2: sp_bacteria

3: sp_fungl:*

4: sp_human:*

5: sp_inverteb:

6: sp_mammal:*

7: sp_mhc:*

8: sp_organel1:

9: sp_phage:*

10: sp_plant:*

11: sp_rodent:

12: sp_vtrus:*

13: sp_vertebr

14: sp_urclass

15: sp_bacteri

17: sp_archeap
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Match
      BLOSUM62
Gapop 10.0 , Gapext 0.5
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1275
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Copyright (c) 1993 - 2002 Compus
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sp_bacteria:*
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sp_unclassified:*
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093XP2
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P93495
082625
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P93494
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Q9FY30	080932	Q9SDZ4	Q9M2S9	Q9FMA0	Q9ZP31	048818	Q9AYR1	Q9FVG9	Q9LLB1	Q9M5I5	Q9FLC5	Q9ZP36	080622	Q38866	Q9M5I7	Q9C554	Q38863	Q9LDR9	Q9FUM2	Q94KT7	049194	Q40636	P93442	Q93XP1	Q946J0	Q946J1	Q9ZP35	022874
Q9fy30	56080	Q9sdz4	Q9m2s	Q9fma0	Q9zp3	048818	Q9ayı	Q9fvg9	Q911b1	Q9m51	Q9fic	Q9zp3	080622	Q3886	Q9m517	Q9c554	Q3886	Q91dr9	Q9fum2	Q94kt7	049194	Q40636	P93442	Q93xp1	Q9461	Q946 j 1	Q9zp:	02287
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01-NOV-1998
01-NOV-1998
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    runus armeniaca (Apricot).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidenesids I; Rosales; Rosaceae: Amurania:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXPANSIN. PA-EXP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-BERGERON; TISSUE-MESOCARP PLUS EXOCARP;
STRAIN-BERGERON; TISSUE-MESOCARP PLUS EXOCARP;
STRAIN-BERGERON; TISSUE-MESOCARP PLUS EXOCARP;
                                     Q9LLB2;
01-OCT-2000 (TrEMBLrel. 15,
01-OCT-2000 (TrEMBLrel. 15,
01-JUN-2001 (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     082093
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ProDom; PD002179; Pollen_allergen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=36596
Eukaryota; Viridiplantae;
                 Zinnia elegans
                             EXPANSIN 2.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000882; Pollen_allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; U93167; AAC33529.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Molecular cloning and nucleotide sequence
from apricot fruit.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144
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(TrembLrel. 08, Last seq
(TrembLrel. 19, Last ann
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  Streptophyta; Embryophyta; Tracheophyta;
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Best Local :
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EMBL; AF230332; AAF35901.1;
InterPro; IPR000882; Pollen_allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids II; Asterales; Asteraceae; Asteroideae;
           wall-modifying enzymes is associated with pectin-related changes the cell wall during ripening of cherry (P. cerasus) fruit."; submitted (FEB-2001) to the EMBL/GenBanK/DDBJ databases.

EMBL: AF297521; AAG13982.1; -.
EMBL: AF350937; AAK48846.1; -.
InterPro; IPR000882; Pollen_allergen.

Pfam: PF01357; Pollen_allergen; 1.
                                                                                                                       SPECIES=P.cerasus;
Yoo S.-D., Gao Z.,
                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2001 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD002179; Pollen_allergen;
SEQUENCE 245 AA; 26201 MW; F66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Heliantheae;
                                                                                                                                                                                                                                                                                           Spermatophyta; Magnoliophyta; eurosids I; Rosales; Rosaceae;
                                                                                                                                                                                                                                                                                                                                  Prunus avium (Cherry), and Prunus cerasus.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9FUM3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI\_TaxID=34245;
                                                                                                          Yoo S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.; "Coordinated expression of genes encoding expansins and other cell
                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                Submitted
                                                                                                                                                                                            Wu Z., Wiersma P.A.;
"Differential Expression
(Prunus avium L.) During
                                                                                                                                                                                                                                      SPECIES=P.avium;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                            NCBI_TaxID=42229, 140311;
                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CNDDPKWCLPGSIVVTATNFCPPNPGLSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGIV 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YGGWENGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGSCYEMR 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PISFQRVPCVKKGGVRFTINGHSYFNLILITNVGGAGDVHSVSIKGSKTGWQSMSRNWGQ 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           196;
 PR01225;
                                                                                                                                                                                (AUG-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Zinnia.
  EXPANSNFAMLY
                                                                                                                                         TISSUE=RIPENING FRUIT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89.3%;
86.7%;
                                                                                                                                                                                                                                                                                                                                                                                           16,
16,
                                                                                                                                                                                            of Expansin Genes Isolated from Sweet Cherry Fruit Ripening.";
                                                                                                                                                                                                                                                                                                                      Streptophyta; Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19;
                                                                                                                                                                                                                                                                                                                                                                                                                       Created)
                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 1138; DB Pred. No. 7e-97;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                           eudicotyledons; core eudicots;
Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F66E26114C27E360 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    254
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
                                                                                                                                                                                  databases
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  cells.";
                                                                                                                                                                                                                                                                                                                         Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                            Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
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Last sequence update)
Last annotation update)

Created)

PRT;

253

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QUENTLY OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COLOR OF THE COL
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Best [
                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO1225; EXPANSNFAMLY.
PRODOM; PD002179; PO11en_allergen; 1.
PROSTITE; PS00030; RRM_RNP_1; UNKNOWN.
SEQUENCE 260 AA; 28266 MW; 32A703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "An second expansin is expressed in chickpea epicotyls."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AJ291817; CAC19184.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-CV. CASTELLANA; TISSUE-ETIOLAT Dopico B., Sanchez M.A., Labrador E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; eudicotyloeurosids I; Fabales; Fabaceae; Papilion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EXPANSIN.

Cicer arietinum (Chickpea) (Garbanzo)

Circer arietinum (Chickpea) (Garbanzo)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9FNTO;
01-MAR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9FNT0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ProDom; PD002179; Pollen_allergen; 1. SEQUENCE 254 AA; 27278 MW; 953A7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR000882; Pollen_allergen
InterPro; IPR000504; RRM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=3827;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae;
                                       181
                                                                                                                    121
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   148
                                                                               154
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                                                                                                                                                            94
                                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                                           Y Match
                                                                                                                                                                                                                                       34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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                                                                                                                                                                                                                                                           1 DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match
                  QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGI 120
                                                                                                                                                                              TCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG
                                                                                                                                                                                                                                         DYGGWEGAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGSCYEM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DYGGWEGAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGSCYEM
QNWQSNSYLNGQPLSFQVTTSDGRTMTSYNVAPSNWQFGQTFQGAQF
                                                                             VPVSFRRVPCMKKGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSIKGSRTGWQSMSRNWG
                                                                                                                                                          RCNDDPRWCKPGSIIVTATNFCPPNPSLANNNGGWCNPPLQHFDMAEPAFLQIAEYRAGI 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VPVTFRRVPCMKKGGIRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQPMSRNWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RCNNDPRWCRPGSIIVTATNFCPPNFAQSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGI
                                                                                                                                                                                                                                                                                                                          196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          197;
                                                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CASTELLANA; TISSUE-ETIOLATED EPICOTYLS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 16, Created)
(TrEMBLrel. 16, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                      88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           86.9%;
                                                                                                                                                                                                                                                                                                                      18;
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                                                                                                                                                                                                                                                                                                                                        Score 1134;
Pred. No. 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 1134;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eptophyta; Embryophyta; Tracheophyta;
eudicotyledons; core eudicots; Rosid
; Papilionoideae; Cicereae; Cicer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                     32A70368ED2883E9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     953A7EB2491FD0E1 CRC64;
                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  260 AA.
                                                                                                                                                                                                                                                                                                                                        DB 10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18;
                                                                                                                                                                                                                                                                                                                      13;
                                                                                                                                                                                                                                                                                                                                                         Length 260;
                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                  180
                                                                                                                                                                                                                                         93
                                                                                                                                                                                                                                                                              60
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                                                                             213
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                                                                                                                                                                                                                                                                                                                      0;
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                                                                                                                                                                                                                                                                                                                                                         RESULT
Q93XP2
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 195;
                                                                                                                                                                                                                                                                                                                  Q93XP2;
                                   TISSUE=RIPENING FRU
YOO S.-D., GAO Z.,
                                                                                                                                                                                           Prunus cerasus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9SBT1;
01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                    EXP1
                                                                                                                                                                                                                                     EXPANSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9SBT1
                                                                          SEQUENCE
                                                                                                                NCBI_TaxID=140311;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=CV.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          independent.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                          206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                      FRUIT;
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RESULT

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Yoo S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.; "Coordinated expression of genes encoding expansins and other cell.wall-modifying enzymes is associated with pectin-related changes in the cell wall during ripening of cherry (P. cerasus) fruit."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosiceurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNEAMLY. Pr0D0m; PD002179; POLLEn_allergen; 1. PROSITE; PS00626; RCC1_2; UNKNOWN_1. SEQUENCE 253 AA; 26887 MW; CE39CF(
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fragaria ananassa (Strawberry).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Kosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plant Physiol. 12:1273-1279(1999). EMBL; AF159563; AAF21101.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Civello P.M., Sabehat A., Powell A.L.T., Bennett A.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro; IPR000882; Pollen_allergen.
InterPro; IPR000408; RCC1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GQNWQSNNYLNGQALSFQVTTSDGRTVTSNNVAPGNWQFGQTFSGGQF
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85.5%;
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRT;
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
081133;
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ProDom; PD002179; Pollen_allergen; 1.
SEQUENCE 252 AA; 26743 MW; BF0B86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Homolog to expansin in peach fruit."; Submitted (JUN-1999) to the EMBL/GenBank/DDBJ EMBL; AB029083; BAB19676.1; -. InterPro; IPR000882; Pollen_allergen.
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Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnollophyta; eudicotyledons;
eurosids I; Rosales; Rosaceae; Amygdaloideae;
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85.5%;
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Last sequence update)
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Pred. No. 1.8e-93;
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          Query Match
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01-NOV-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                               SEQUENCE
                                                                                                                                                                                                                                                                               exogenous auxin."
                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXPANSIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P93493;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=3352;
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                                                                    232 AA;
                85.
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Interpro; IPR000882; Pollen_allergen. Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNEAMLY. ProDom; PD002179; Pollen_allergen; 1. SEQUENCE 252 AA; 26758 MW; 5E81AE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mbeguie-A-Mbeguie D., Fils-Lycaon B.;
"Molecular cloning and nucleotide sequence of
from apricot fruit.";
Submitted (DEC-1997) to the EMBL/GenBank/DDBJ
EMBL, AF038815; AAC33530.1; -
                                                                                                                                                                                                                                                                                                            Pinus taeda (Loblolly pine).
Eukaryota; Viridiplantae; Stre
Spermatophyta; Coniferopsida;
                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-1997 (TrEMBLrel.
01-MAY-1997 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Prunus armeniaca (Apricot).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheor Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                  TISSUE-HYPOCOTYL;
Hutchison K.W., Singer P.B.,
"Expansins are conserved in o
                                                                    PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen;
                                                                                                        InterPro; IPR000882; Pollen_allergen
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                              Submitted (JUL-1996) to the EMBL/GenBank/DDBJ EMBL; U64891; AAB40635.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60 MTCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DY-GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MRCDSDPKWCLPGSIIVTATNFCPPNLAQSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAG
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                                    24745 MW;
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84.6%;
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03, Last sequence 19, Last annotations
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08, Last sequ
19, Last anno
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Pred. No. 6
                                                                                                                                                                                                                       Diaz-Sala
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                cptophyta; Embryophyta;
Coniferales; Pinaceae;
                                      1340B0573DE907CF CRC64;
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1092;
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and expressed
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                                                                                                                                                                                                                       Greenwood M.
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                                                                                                                                                                                                                                                                                                                                   Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          227
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Best Local Similarity

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Best Local
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P93492 PRELIMINARY; PRT;
P93492;
01-MAY-1997 (TrEMBLrel. 03, Created)
                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PRO1225; EXPANSNFAMLY.
PRODOM; PD002179; POllen_allergen; 1.
SEQUENCE 253 AA; 27150 MW; 2675BB1569BD75D4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                               Hutchison K.W., Singer P.B., McInnis S., Diaz-Sala C., "Expansins are conserved in conifers and expressed in response to exogenous auxin.", Plant Physiol. 120:827-832(1999).

EMBL: AF085330; AAD47901.1; -
InterPro; TPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.

PRINTS: DR01375; PROAUSURDAMIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-HYPOCOTYL;
MEDLINE-99329318; PubMed-10398718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Stro
Spermatophyta; Coniferopsida;
                                                                                                             208
                                                                                                                   182 NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGFQ 226
                                                                                                                                                                    148
                                                                                                                                                                                     122 PVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID-3352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pinus taeda (Loblolly pine).
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                                                                                                                                                                                                                88 CNDDPQWCLPGTVTVTATNECPPNNALPNDNGGWCNPPLQHEDMAEPAFLKIAKYRGGIV 147
                                                                                                                                                                                                                                          62 CTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIV 121
                                                                                                                                                                                                                                                                       28 YGGWESAHATFYGGSDASGTMGGACCYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187 NWQSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSNWQFGQTFEGSQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 NWOSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQ 226
                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                      2 YGGWQSGHATEYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           62 CTNDPKWCLPGTIRVTATNECPPNEALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIV 121
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                                                                                                                                                         NWQSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSNWQFGQTFEGSQ 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YGGWESAHATFYGGSDASGTMGGACGYCNLYSQGYGTNTAALSTALFNDGLSCGACYEMR 66
                                                                                                                                                                                                                                                                                                                                          186;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CNDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIV 126
                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                85.6%; Score 1092; DB 10; Length 253; 82.7%; Pred. No. 1.2e-92;
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lda; Coniferales; Pinaceae;
                                                                                                                                                                                                                                                                                                                                       22;
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                                   232
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Best Local Similarity
        Matches 185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                               InterPro; IPR000882; Pollen_allergen. Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNEAMLY.
                                                                                                                                                                                   "Expansins are conserved in conffers and expressed in response exogenous auxin.".

Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                     Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases EMBL; U64893; AAB40637.1; -.
                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 03, Created)
01-MAY-1997 (TrEMBLrel. 03, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                         SEQUENCE
                                                                                          NON_TER
                                                                                             ProDom; PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                   TISSUE-HYPOCOTYL;
                                                                                                                                                                                                                                                                                                                  Spermatophyta; Coniferopsida;
                                                                                                                                                                                                                                                                                                                                               Pinus taeda (Loblolly pine).
                                                                                                                                                                                                                                                                                                                                                                   EXPANSIN (FRAGMENT)
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3352;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    P93495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exogenous auxin.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U64890; Am840634.1;
InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pinus taeda (Loblolly pine).

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pinus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR01225; EXPANSNFAMLY.

ProDom; PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-1997 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              187 NWQSNSYLNGQSLSFQYTTSDGRTIVSNNVAPSNWQFGQTFEGSQ 231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hutchison K.W., Singer P.B., Diaz-Sala C., Greenwood M.S., "Expansins are conserved in conffers and expressed in response to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-HYPOCOTYL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        122 PVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         62 CTNDPKWCLPGTIRVTATNECPPNEALPNDDGGWCNPDLQHEDMAEDAFLQTAQYRAGIV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      7 YGGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMR 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 YGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMT 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVHAVSIKGSMSGWQPMSRNWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNDDPQWCLPGTVTVTATNECPPNNALPNDNGGWCNPPLQHEDMAEPAFLKIAKYRGGIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   185;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        h 85.3%; Score 1087; DB 10; Length 232; Similarity 82.2%; Pred. No. 3.2e-92;
                                                                     232 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       232 AA; 24734 MW; 1340AF483DE0741F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                24694 MW; 9238EACD9E1F6C5E CRC64;
85.1%; Score 1085; DB 10
82.2%; Pred. No. 4.9e-92;
tive 23; Mismatches 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03, Last sequence update)
19, Last annotation update)
                                                                                                                                                                                                                                                                                                                         Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
                                                                                                                                                                                                                                                                                                             Coniferales; Pinaceae; Pinus
                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                               232 AA.
                             DB 10; Length 232;
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    082625
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Eycopersicon esculentum (Tomato).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Catala C., Rose J.K.C., Bennett A.B.; "Hormonal_regulation and expression patterns of LeExP2, a new tomato
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EXPANSIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000882; Pollen_allergen
pfam; pf01357; Pollen_allergen; 1.
prINTS; pr01225; EXPANSURFAMIX.
proDom; pD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; AF096776; AAC64201.1; -
EMBL; AJ239068; CAB43197.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. VFN8
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                                                                181 QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
                                                                                                                                                                     141 VPVSFRRVPCMRKGGIRFTVNGHSFFNLVLVTNVGGAGDIQSVSIKGSNTGWQAMSRNWG
                                                                                                                                                                                                                                                                                                                                                                                81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 60
CNDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIV 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           YGGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQ 226
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                                                                                                                                                                                                                                                                     VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTNDEKWCLEGTIRVTATNECEPPNFALPNDDGGWCNPPLOHEDMAEPAFLQIAQYRAGI 120
                                                                                                                                                                                                                                                                                                                                                                                      TCNNAAQWCLQGTITVTATNFCPPNPSLPNNNGGWCNPPLQHFDLAQPAFLQIAKYKAGI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            85.0%; Score 1084; DB 10; 81.9%; Pred. No. 6.6e-92;
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RESULT 15
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Search completed: October 11, Job time: 20.6007 secs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q9SWD4;
Q9SWD4;
Q1-MAY-2000
Q1-MAY-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Vriezen W.H., De Graaf B., Mariani C., Voesenek L.A.C.J.; "Submergence induces expansin gene expression in flooding-tolerant Rumex palustris and not in flooding-intolerant R. acetosa."; planta 210:956-963 (2000).
EMBL, AF167360; AAD49956.1; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Caryophyllidae; Caryophyllales; Polygonaceae; Rumex.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXP1
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pfam; PF01357; Pollen_allergen; 1.

prINTS; PR01225; EXPANSNFAMLY.

proDom; PD002179; Pollen_allergen; 1.

SEQUENCE 253 AA; 27063 MW; 7DC75610C80B23A8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Rumex palustris
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=20330988; PubMed=10872228;
                                                                                                                                                                                                                                                                                     146 IVPVSFRRVPCGRKGGIRFTVNGHSYFNLVLITINVGGAGDVHSVSIKGSRGGWQAMSRNW 205
                                                                                                                                            206 GQNWQSNSYLKGQSLSFMVTTSDGRTLTSFNVAPFKWQFGQTFEGSQF 253
                                                                                                                                                                                  180 GQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
                                                                                                                                                                                                                                                                                                                                                     120 IVPVSERRVPCMKKGGVRETINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                 86 INCTROPRWCIGGVITVTATNFCPPSFALANNNGGWCNPPLQHFDLAEPAFLQIAQYHAG 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26 DYGGDWNGGHATFYGGGDASGTMGGACGYGKLYSQGYGTSTAALSTALFNNGLSCGACFE 85
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 DYGG-WOSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFE 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      253 AA;
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82.9%; Pred. No. 1.1
                                             2002, 14:59:43
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Result
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Maximum Match 100%
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Maximum DB seq length: 2000000000
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Perfect score:
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          Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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1275
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        SwissProt_40:*
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Copyright (c) 1993 - 2002 Compugen Ltd
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MPLI_CYNDA
MPAI_PHANIZE
GUNZ_MAIZE
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FBNI_BOVIN
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               Q9tv36
P048410
P48410
Q9rmg3
Q02958
Q02958
P19470
P35908
P35908
P373775
P29025
Q99250
P05790
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             6 sus scrofa
9 dallus gall
0 drosophila
1 bacillus th
1 ovis aries
9 schistosoma
1 schistosoma
1 schistosoma
2 schistosoma
3 homo sapien
5 gallus gall
5 rhizopus ni
6 homo sapien
6 bombyx mori
8 bos taurus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    phleum
holcus
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A55390.1; HHO. HHO. B882; POllen_allergen; EXPANSNFAMLY. POLLen_allerge; EXPANSIN_CEB; EXPANSIN_EG45; EXPANSIN_EG45; FOLLE1;	N.A. 25; PubMed=793 enta R., Vrtal uchene M.; DNA cloning o pratense); rec ens from elght n. Immunol. 94 R LOCATION: Se BELONGS TO T CONTAINS 1 E CONTAINS 1 E CONTAINS 1 E CONTAINS 1 S CONTAINS 1 E CONTAINS 1 S C	p 1 mmon antae oliop	2, Cr 2, La 1, La	ANDARD;	571 465 1325 283 283 499 680 1456 373 3873
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Query Match
Best Local Similarity
Matches 67; Conserv

Conservative

18.2%; Score 231.5; DB 1; Length 263; 27.6%; Pred. No. 6.2e-13; tive 41; Mismatches 96; Indels 39

39;

Gaps

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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Major pollen allergen Hol 1 1 precursor (Hol 1 I) (Hol 1 1.0101
                                                                                                                                                                                                             STRAIN-CV. AVENEAE; TISSUE-Pollen;
MEDLINE-96319506; PubMed-8768803;
Schramm G.D., Petersen A., Bufe A., Schlaak M., Becker W.M.;
Schramm G.D., Petersen A., Bufe A., Schlaak M., Becker W.M.;
"Identification and characterization of the major allergens
grass (Holcus lanatus), Hol 1 1 and Hol 1 5.";
Int. Arch. Allergy Immunol. 110:354-363(1996).
-i- SUBCELLULAR LOCATION: Secreted.
-i- SUBLIARITY: DELONGS TO THE LOL P I FAMILY OF ALLERGENS.
-i- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-i- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Mapping of IgE-binding epitopes on the recombinant major allergen of velvet grass pollen, rHol 1 l.";

T. Allergy Clin. Immunol. 99:781-787(1997).
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Holcus lanatus (Velvet grass).
Eukaryota; Viridiplantae; Stre
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                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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EMBL; Z68893;
HSSP; P43214;
                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                     modified and this statement is not removed.
                                                                                                                     the European Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
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                                  EMBL; Z27084; CAA81610.1; -.
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                      CAA93121.1;
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A., Becker W.M., Schlaak M.;
b) to the EMBL/GenBank/DDBJ databases
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                                                                                                            Usage by
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Pfam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSIFAMIX;
ProDom; PD002179; Pollen_allergen; 1.
PROSITE; PS50843; EXPANSIN_CBD; 1.
PROSITE; PS50843; EXPANSIN_EG45; 1.
Allergen; Signal.
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01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 19, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-last annotation update)

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                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.

MEDLINE-90375479; PubMed-1697854;

Perez M., Ishioka G.Y., Walker L.E., Chesnut R.W.;

Perez M., Ishioka G.Y., Walker L.E., Chesnut R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Poeae; Lolium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4522;
  MEDLINE=86242068; PubMed=3718469;
                           TISSUE-Pollen;
                                                    SEQUENCE OF 24-53.
                                                                                                                       rye-grass pollen
                                                                                                                                                                         Knox R.B.
                                                                                                                                                                                           Avjoglu A., Davies S., Hough T., Singh
                                                                                                                                                                                                                 Griffith I.J., Smith P.M., Pollock J.,
                                                                                                                                                                                                                                             MEDLINE=91160716; PubMed=2001733;
                                                                                                                                                                                                                                                                   TISSUE=Pollen;
                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A., AND SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                      J. Biol. Chem.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142
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                                                                                                                                              "Cloning and sequencing of Lol pI,
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27.6%;
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EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
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EMBL; M57476; AAA63278.1; -.
PIR; A23341; A23341.
PIR; B37881; B37881.
PIR; S13614; S13614.
HSSP; P43214; 1WHO.
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                                                                                                                                                                                                                                                                         CONFLICT
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SEQUENCE
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- ID SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
- I- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
- I- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS50842; EXPANSIN_CBD; 1.
PROSITE: PS50842; EXPANSIN_EG45; 1.
Allergen; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000882; Pollen_allergen
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Physicochemical and immunochemical characterization of allergenic proteins from rye-grass (Lolium perenne) pollen prepared by a rapio and efficient purification method.";
                                                                                                                                                                                                                                                                                                                                                                                                                              CHAIN
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"Isolation and characterization of
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                                                                                                                                                               36 EYGDKWLDAKSTWYGKPTGAGPKDNGGACGYKNVDKAPFNGMTGCGNTPIFKDGRGCGSC
                                                                                                                                                                                        1 DYGG-WQSGHATFYGGGDASGTM--GGACGYGNLYSQGYGTNTVALSTALFNNGLSCGAC
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IKEKGKDKWIELKESWGAVWRIDTPDKLTGP-FTVRYTTEGGTKSEFEDVIPEGWKADTS
                        IK-GSRTGWQSMSRNWGQNWQ--SNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQT
                                                   KGEEQNVRSAGELELQFRRVKCKYPDDTKPTFHVEKASNPNYLAILVKYVDGDGDVVAVD
                                                                                                        FEIKCTK-PESCSGEAVTVTIT-------DDN---EEPIAPYHFDLSGHAFGSMAK
                                                                                                                                  FEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPL--QHFDMAEPAFLQIAQ 115
                                                                             ----YRAGIVPVSFRRVPCMKKGGVRFTINGHSYFN----LVLITNVGGAGDVHSVS
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8; Mismatches
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EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC. . .) (POTENTIAL).
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P -> C (IN REF. 3).
P -> C (IN REF. 3).
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7675896F279C88C9 CRC64;
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Best Local S
Matches 65
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16-0CT-2001
16-0CT-2001
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i- SUBCELLULAR LOCATION: Secreted.

-i- DISEASE: CAUSES GRASS POLLEN ALLERGY.

-i- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MPC1
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                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Smith P.M., Suphioglu C., Griffith I.J., Theriault K., Knox R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC Chloridoideae; Cynodonteae; Cynodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cynodon dactylon (Bermuda grass).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Major pollen allergen Cyn
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                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01357; Pollen_allergen; PRINTS; PR01225; EXPANSNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96347957; PubMed-8757211;
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                                                                                                                                                                                                                                                                                                                                                           ProDom; PD002179; Pollen_allergen;
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IKGSRTG-WQSMSRNWGQNWQSNNYLNGQG-LSFQVTLSDGRTLTAYNLVPSNWQFGQTY 222
                                                                                                              FEMTCTNDPKWCL--PGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQLAQ 115
                            KGQEDKLRKAGELTLQFRRVKCKYPSGTKITFHIEKGSNDHYLALLVKYAAGDGNIVAVD 178
                                                       -----YRAGIVPVSFRRVPCMKKGGVRFTIN----GHSYFNLVLITNVGGAGDVHSVS 164
                                                                                                                                         YGSKWLEARATFYGSNPRGAAPDDHGGACGYKDVDKPPFDGMTACGNEPTFKDGLGCRAC 73
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                                                                                                                                                                                                                                                                                                                                                                                                       IPR000882; Pollen_allergen.
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(Rel. 40,
(Rel. 41,
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159
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EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                 Score 225; DB 1;
Pred. No. 2.1e-12;
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Suphioglu C., Singh M.B.;
"Cloning, sequencing and expression and four isoforms of Pha a 5, the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Major pollen allergen Pha a 1 precursor (Pha a I).
Phalaris aquatica (Canary grass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                      DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                   Aliergen;
                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE;
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MEDLINE=93319091; PubMed=7687099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=28479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Poeae; Phalaris
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q41260;
                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                      42
         58 FEMTCTNDPKWCL--PGTIRVTATNFCPPNFALPNDDGGWCNPPL--QHFDMAEPAFLQI 113
                                                                                                                                                                Local
                                                                                                 1
                                                                                               DYGG-WQSGHATFYGGGDASGTM--GGACGYGNLYSQGYGTNTVALSTALFNNGLSCGAC
                                                      EYGDKWLDAKSTWYGKPTGAGPKDNGGACGYKDVDKAPFNGMTGCGNTP1FKDGRGCGSC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Exp. Allergy 25:853-865(1995)
                                                                                                                                                                                                                                                                                                                                                                                                                                                PR01225; EXPANSNFAMLY. PD0002179; Pollen_aller
                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       PS50843;
PS50842;
                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein;
                                                                                                                                                                                                                              30
67
187
38
37
269
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(Rel.
(Rel.
                                                                                                                                            Conservative
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                                                                                                                                                                                                                                AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                       EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35,
                                                                                                                                                                                                                                                                                                                                                                                                                          EXPANSIN_CBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pollen_allergen; 1.
                                                                                                                                                                                                                                                         269
173
268
38
37
                                                                                                                                                                                                                           29011 MW;
                                                                                                                                                                17.0%;
26.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                                                                                                                                                                                                                                                                                                                                                                                 Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression in Escherichia coli of Pha a l a 5, the major allergens of canary grass
                                                                                                                                            42;
                                                                                                                                                                Pred
                                                                                                                                                                                     Score 216.5;
                                                                                                                                                                                                                              EXPANSIN-LIKE EG45.
                                                                                                                                                                                                                                                                                                                                          MAJOR POLLEN ALLERGEN PHA A 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                          ed. No. 1.2
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            269
                                                                                                                                          1.2e-11;
ches 93;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   There are no restrictions ong as its content is in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A
                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Usage
                                                                                                                                                                                                                                                                    . .) (POTENTIAL)
                                                                                                                                                                                                                                  CRC64;
                                                                                                                                          Indels
                                                                                                                                                                                  Length
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                                                                                                                                                                                       269;
                                                                                                                                            39;
                                                                                                                                          Gaps
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                                                      101
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                           Matches
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                                          Best
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-!- SIMILARITY: |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           _ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning, expression and immunological characterization of Ory s the major allergen of rice pollen."; Gene 164:255-259(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MPO1
                                                                                                                                                     PROSITE; PS50842; EXPANSIN_CBD; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
Allergen; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Oryza sativa (Rice).
Eukaryota; Viridiplantae;
                                                                               SEQUENCE
                                                                                             CARBOHYD
                                                                                                         DOMAIN
                                                                                                                    DOMAIN
                                                                                                                                  CHAIN
                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                      HSSP; P43214;
                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                       entities
                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. Tuse by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                           between
                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- TISSUE SPECIFICITY: EXPRESSED IN MATURE ANTHERS VEGETATIVE OR OTHER FLORAL TISSUES.
-!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bhalla P.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Xu H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=96069591; PubMed=7590339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Major pollen allergen Ory s 1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1997
01-MAR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q40638;
                                                                                                                                                                                                 ProDom; PD002179;
                                                                                                                                                                                                            PRINTS; PRO1225; EXPANSNFAMLY
                                                                                                                                                                                                                                                               EMBL; U31771; AAA86533.1; -
                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Anther
                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      163 VSIK-GSRTGWQSMSRNWGQNWQ--SNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   102 FELKCSK-PESCSGEPITVHITDDN--
 23 GGACGYGNLYSQGY-GTNTVALSTALFNNGLSCGACFEMTCTNDPKWC--LPGTIRVTAT 79
                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORYSA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VDIKEKGKDKWIELKESWGAIWRIDTPDKLTGP-FTVRYTTEGGTKAEFEDVIPEGWK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AKKGEEENVRGAGELELQFRRVKCKYPDGTKPTFHVEKGSNPNYLALLVKYVDGDGDVVA 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AQ-----YRAGIVPVSFRRVPCMKKGGVRETIN----GHSYFNLVLITNVGGAGDVHS 162
                                                                                                                                                                                                                          PF01357; Pollen_allergen;
                            59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Theerakulpisut P.,
                                                                                                                                                                                                                                                                                                      requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                           the Swiss Institute of Bioinformatics
                                                                                                                                                                                                                                        IPR000882; Pollen_allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 35, (Rel. 35, Rel. 41,
                                                                               263 AA;
                            Conservative
                                                                                                                                                                                                                                                      1WHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                BELONGS TO THE LOL P I FAMILY OF ALLERGENS CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                   Pollen_allergen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 35, Created)
                                                                                                       263
164
259
                                                                                 28497 MW;
                                       15.1%;
28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Goulding N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae;
                        36;
                                         Pred.
                                                     Score
                                                                                             N-LINKED (GLCNAC
                                                                                                       EXPANSIN-LIKE EG45
EXPANSIN-LIKE CBD.
                                                                                                                                 MAJOR POLLEN ALLERGEN
                                                                                                                                              POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                               B1C5F24EA398DD60 CRC64;
                            Mismatches
                                       2 192.5;
1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Suphioglu C., Singh M.B.,
                           .4e-09;
nes 77;
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                                                                                                                                                                                                                                                                                                                                 as its content
                                                      DB 1;
                                                                                                                       EG45
                                                                                                                                                                                                                                                                                                                      Usage
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                                                                                                                                                                                                                                                                                                                                                           and the EMBL outstation
                                                     Length
                           Indels
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                                                      263;
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                                                                                                                                                                                                                                                                                                                                                                          collaboration
                                                                                                                                                                                                                                                                                                                                  'n
                            Gaps
                                                                                                                                                                                                                                                                                                                       commercial
                                                                                                                                                                                                                                                                                                                                    no
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Дb

61

GGACGYKDVDKAPFLGMNSCG-NDPIFKDGKGCGSCFEIKCSK-PEACSDKPALIHVTDM 118

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                                                  Matches
                                                                               Query Match
                                                                                                                                                                 ProDom: PD002179; Pollen_allergen: 1.
PROSITE: PS50843; EXPANSIN_CBD: 1.
PROSITE: PS50842; EXPANSIN_EG45; 1.
                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                          EMBL; L14271; AAA33496.1;
PIR; JC1524; JC1524.
HSSP; P43214; IWHO.
                                                                                                                                                   Allergen; Multigene family.
                                                                                                                                                                                                                                                                                                                                            modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                            DOMAIN
                                                                                                                                                                                                                 Pfam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
                                                                                                                                                                                                                                                              MaizeDB; 65840;
                                                                                                                                                                                                                                                                                                                                    or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                     use
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation updat
Pollen allergen Zea m 1 (Zea m I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bedinger P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-94010312; PubMed-8406014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Pollen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zea mays (Maize).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-4577
40 TVALSTALENNGLSCGACFEMTCTNDPKWCL--PGTIRVTATNFCPPNFALPNDDGGWCN 97
                                                                  Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             222 PKPLKGPFSVRVTTEGARRSSAEDAIP 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           188 YLNGQG-LSFQVTLSDGRTLTAYNLVP 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       119 N-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 NFCPPNFALPNDDGGWCNPPL--QHFDMAEPAFLQIAQ----YRAGIVPVSFRRVPCMKK 133
                                                                                                                                                                                                                                                                                                                                                                                             European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN. SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEVELOPMENTAL STAGE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE SPECIFICITY: POLLEN TISSUE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                grass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DISEASE: CAUSES MAIZE POLLEN ALLERGY.
                                                                                                                                                                                                                                                                                                                                                                          SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLLEN MITOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     mI, the maize homolog of the allergen encoding Lol pI gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     _MAIZE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADTKITFHIEKASNPNYLALLVKYVAGDGDVVEVEIKEKGSEE-WKALKESWGAIWRIDT 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GGVRFTIN----GHSYFNLVLTTNVGGAGDVHSVSI--KGSRTGWQSMSRNWGQNWQSNN 187
                                                                  Similarity
                                                                                                                                                                                                                                           IPR000882; Pollen_allergen
                                                                                                             191 AA;
                                                  Conservative
                                                                                                                           105
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -----DEPIAAYHFDLSGLAMAKDGKDEELRKAGIIDTQFRRVKCKYP 162
                                                                                                           21362 MW;
                                                               14.5%; Score
26.3%; Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EXPRESSION LOW BEFORE AND HIGH AFTER
                                               36;
                                                                                                                      EXPANSIN-LIKE EG45.
                                                                            Score 185;
                                                                                                        6E2A9DF921C45C63 CRC64;
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                                                 Mismatches
                                                             No. 4.2e-09;
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                                                                             DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN.
                                                                          Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Poaceae; PACC clade;
                                            Gaps
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RESULT 8
GUN5_TRIRE
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                  CARBOHYD
DISULFID
                                                                                                                                         PROSITE: PS00562; CBD_FUNGAL; 1.
PROSITE: PS50842; EXPANSIN_EG45; 1.
PROSITE: PS501140; GLYCOSYL_HYDROL_F45; 1.
Cellulose degradation; Hydrolase; Glycosi.
SIGNAL 1 17
POTENTIAL.
                                                                                                                                                                                                                                    InterPro; IPR000254; CBD_fungal.
InterPro; IPR000334; Glyco_hydro_45.
Pfam; PF00734; CBD_1; 1.
Pfam; PF02015; Glyco_hydro_45; 1.
ProDom; PD001821; CBD_fungal; 1.
                                                                                                                               CHAIN
     DISULFID
                                                                  DOMAIN
                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                     DOMAIN
                                                                                                                                                                                                                               SMART; SM00236; fCBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                             EMBL; Z33381; CAA83846.1; -. HSSP; P00725; 2CBH.
                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                isolated by expression in yeast.";
Mol. Microbiol. 13:219-228(1994).
-i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saloheimo A., Henrissat B., Hoffren A.-M., Tele
"A novel, small endoglucanase gene, eg15, from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=QM9414 / RUT C-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Trichoderma reesei (Hypocrea jecorina).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
Hypocreales; Hypocreaceae; Hypocrea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=95075308; PubMed=7984103;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 )1-NOV-1995 (Rel. 32, Createu)
)1-NOV-1995 (Rel. 32, Last sequence update)
)1-SC-1998 (Rel. 37, Last annotation update)
15-DEC-1998 (Rel. 37, Last annotation update)
Endoqlucanase V_precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P43317
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILÁRITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         linkages in cellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -LVLITNVGGAGDVHSVSIKGSRTG-WQSMSRNWGQNWQSNNYLNGQG-LSFQVTLSDGR 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ---YHFDLSGKAFGSLAKPGLNDKLRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGCNPNY 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PPLQHEDMAEPAFLQIAQ-----YRAGIVPVSFRRVPCMKKGGVRFTINGHSYFN---
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                    PRO/SER-RICH (LINKER).
CELLULOSE-BINDING (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL).
BY SIMILARITY.
BY SIMILARITY.
                                                                              CATALYTIC
                                                                                          PROTON DONOR (BY SIMILARITY).
                                                                                                          NUCLEOPHILE (BY SIMILARITY)
                                                                                                                               ENDOGLUCANASE V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                          Glycosidase;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Teleman O., Penttilae M.;
from Trichoderma reesel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sordariomycetes;
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                                                                                                                                                                                                                                                                                                                       entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Chlamydia trachomatis.";
Science 282:754-759(1998).
-i- SIMILARITY: BELONGS TO THE CHLAMYDIAL CPN0441/CT007/TC0275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stephens R.S., Kalman S., Lammel C.J., Fan J., Marathe R., Aravind L., Mitchell W.P., Olinger L., Tatusov R.L., Zhao Q., Koonin E.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=D/UW-3/CX;
MEDLINE=99000809; PubMed=9784136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chlamydia trachomatis.
                                                                                                                                                                                                                                                                            Hypothetical SEQUENCE 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Davis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=813;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hypothetical protein CT007
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                         EMBL; AE001275; AAC67597.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of an obligate intracellular pathogen of humans:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              136 -- MAQNEIFGDNVVVDFEPIAC 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          111 LQIAQYR--AGIVPVSFRRVPC 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14 GGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNN-----GLSCGACFEMTCTNDPK 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88
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                                                           163 VSIKGSRTGWQSMSRNWGQNWQSNNYLNGQGLSF--QVTLSDGRTLTAYNLVPSNWQFGQ 220
                                                                                                                        103 FDMAEPAFLQIAQYRAGIVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
   221 TYEG 224
                                                                                                                                                                                   43 LSTALENNGLSCGACFEMTCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQH 102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CSSCGTGGAAGQSIIVMVTNLCP-----NNGNAQWC--PVVGGTNQYGYSYHEDI----
                                SRYLGAEVSWKSSKELQDTDLQAVGYFAFQDKSFYQYITLSVG----AYTLALTNWQWSV 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              41;
                                                                                                                                                        LSTPIYIVGDACG-----KDRDEYKNPPLRA 41
                                                                                           FSF-ESQFLQIEN-----AKFKTLP----DQSLRYRQADTSLFATIPVTEM--SGFLLS
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                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           242 AA;
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                                                                                                                                                                                                                                                                                316 AA;
                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                             protein;
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                                                                                                                                                                                                                                                                                35637 MW;
                                                                                                                                                                                                                                     23.9%;
                                                                                                                                                                                                                                                7.9%; Score 100.5;
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5637 MW; 904D2CC28F5CB06E CRC64;
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                                                                                                                                                                                                                     22;
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                                                                                                                                                                                                                                     Pred
                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                   No. 0.12;
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                                                                                                                                                                                                                                                  DB 1; Length 316;
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                        CATJ_MOUSE
                                                          RESULT 11
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P82186;
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"Purification, characterization and amino-acid sequence analysis of a thermostable, low molecular mass endo-beta-1,4-glucanase from blue mussel, Mytilus edulis.";
Eur. J. Biochem. 267:4970-4977(1999).
Eur. J. Biochem. 267:4970-4977(1999).
-i- FUNCTION: ACTIVE TOWARDS THE SOLUBLE CARBOXYMETHYLCELLULOSE (CMC).
-POSSESSES EXPANSIN ACTIVITY TOO.
-i- CAPALLYIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 41, Last annotation update)
101-MAR-2002 (Rel. 41, Last annotation update)
101-MAR-2002 (Rel. 41, Last annotation update)
101-MAR-2003 (Rel. 41, Last annotation update)
101-MAR-2003 (Rel. 40, Created)
103-MAR-2003 (Rel. 40, C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS01140; GIYCOSYL_HYDROL_F45; FALSE_NEG.
Cellulose degradation; Hydrolase; Glycosidase.
ACT_SITE 24 24 NUCLEOPHILE (BY SIMILARITY).
ACT_SITE 132 132 PROTON DONOR (BY SIMILARITY).
DISULFID 4 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida;
Mytiloidea; Mytilidae; Mytilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linkages in cellulose.

-:- TISSUE SPECIFICITY: DIGESTIVE GLAND.
-:- MASS SPECTROMETRY: MW=19702; METHOD-MALDI.
-:- MISCELLANEOUS: Has an isoelectric point of 7.6. Its optimum pH is 4.6 and optimum temperature is between 30-50 degress celsius.
-:- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Digestive gland;
MEDLINE=20389517; PubMed=10931178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
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CATJ_MOUSE
                                                                                                                                                    143
                                                                                                                                                                                                                                                                                                                             104
                                                                                                                                                                                                  163 VSIKGSRTGWQSMSRNWGQNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQ 220
                                                                                                                                                                                                                                                                                                                                                                                     65
                                                                                                                                                                                                                                                                                                                                                                                                                                            51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 SGHATFYGGGDASGTMG-----GACGYGNL----YSQGYGTNTVALSTALFNN-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYDROLASES)
                                                                                                                                                                                                                                                                                                                       DMAEPAFLQIAQYRAGIVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNV-GGAGDVHS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                         -GLSCGACFEMTCTNDPKWCLPGTIR-----VTATNFCPPNFALPNDDGGWCNPPLQHF 103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SGNPRRYNGKSCASTINYHDSHKGACGCGPASGDAQFGWNAGSFVAAASQMYFDSGNKGW 64
                                                                                                                                                    MGWNNPETTWEVVNCDSEHN-----
                                                                                                                                                                                                                                                                                                                                                                                  CGQHCGQCIKLTTTGGYVPGQGGPVREGLSKTFMITNLCPNIY--PNQD--WCN----- 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                      OGSQY .
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   STANDARD;
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178
157
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7.6%; Score 97.5; DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21; Mismatches
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            333 AA
                                                                                                                                                          -----HDHRT-----PSNSMYGQ 175
                                                                                                                                                                                                                                                                            ---GGHNKYGYELHLDLENGRSQVTG 142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AΑ
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Q9R014; Q9WV51;

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                                                                                                     Matches
                                                                                                                                                  Query Match
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                                                                                                                                                                                                SEQUENCE
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                                                                                                                                                                                                                                                                 CARBOHYD
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115 DYKDWREEGYVTPVRNQGKCGSCWAFAAAGAIEGQMFWKTGNLTPLSVQNLLDCSKTVGN 174
                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00639; THIOL_PROTEASE_HIS; PROSITE; PS00640; THIOL_PROTEASE_ASN;
                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; Thiolprot_act_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AF136272; AAF13142.1; -. EMBL; AF158182; AAD41898.1; -. HSSP; P07711; 1CJL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6J; TISSUE-Embryo; MEDLINE-99456833; PubMed-10526153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with a placenta-restricted expression.";
FEBS Lett. 459:299-304(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tisljar K., Deussing J., Peters C., "Cathepsin J, a novel murine cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/6; TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
7m+hensin J precursor (EC 3.4.22.-) (Cathepsin P) (Catlrp-p).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                        Score 96;
Pred. No.
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                                                                                                                                                                                       F9A8FF1D5A13B721 CRC64;
                                                                                             Mismatches
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                                                                                                                                      DB 1;
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                                                                                                                                                EMBL;
HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gibson M.A., Hatzinikolas G., Kumaratillake J.S., Sandberg L.B., Nicholl J.K., Sutherland G.R., Cleary E.G.;
"Further characterization of proteins associated with elastic fiber microfibrils including the molecular cloning of MAGP-2 (MP25).";
J. Biol. Chem. 271:1096-1103(1996).
                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tilstra D.J., Potter K.A., Byers P.H.;
"Sequence of the coding region of the bovine fibrillin cDNA and localization to bovine chromosome 10.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96132851; PubMed=8557636;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PARTIAL SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 23:480-485(1994).
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Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoldea;
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01-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               266 PNCSSYFVNHAVLVVGYGSEGDV-----KDGNNYW-LIKNSWGEEWGMNGYM 311
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175 KGCQS-GTAHQAFEYYLKNKGLEAEATYPYEGKDGPCRYRSENASANITDYVNLPPN---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31 LYSQGYGTNTVALSTALENNGLSCGACFEMTCTNDPKWCLPGTIRVTATNF--CPPNFAL
                                                                                                                                                                                                                                                                                                                                                                        Biol. Chem. 271:1096-1103(1996).

FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS THAT BINDS CALCIUM. FIBRILIN-1-CONTAINING MICROFIBRILS PROVIDE LONG-TERM FORCE BEARING STRUCTURAL SUPPORTER WITH OTHER PIM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 7 TGF-BETA BINDING PROTEIN DOMAINS.
                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: CONTAINS 43 CALCIUM-BINDING AND 4 NON-CALCIUM BINDING EGF-LIKE DOMAINS.
                                                                                                                                                  P35555;
                                                                                                                                                               L28748; AAA74122.1; -.
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                                                                        IPRO00152; Asx_hydroxyl.
IPRO00561; EGF-like.
IPRO01881; EGF_Ca.
IPR001438; EGF_II.
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34, Last seq
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PRINTS; PR00010; EGFBLOOD. SMART; SM00179; EGF_CA; 42

Pfam; PF00008; EGF; Pfam; PF00683; TB; PRINTS; PRO0010;

InterPro;

InterPro; InterPro; InterPro;

IPR002212;

EGF; 46.

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Pfam; PF00008; EGF; 46.
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SMART; SM00179; EGF_CA; 42.
SMART; SM00101, EGF_Like; 4.
SMART; SM00001; EGF_Like; 4.
PROSITE; PS00010; ASX_HYDROXYL; 43.
PROSITE; PS00022; EGF_1; 2.
PROSITE; PS01186; EGF_2; 38.
PROSITE; PS01187; EGF_CA; 45.
EXCITACELLular matrix; Calcium-binding; Glycoprotein; EGF-like domain; Repeat; Signal; Multigene family.
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Q61554; Q60826;
Q1-NOV-1997 (Re)
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InterPro; IPR001881; EGF_Ca.
InterPro; IPR002212; TB.
                                                                                                                                                                                                                                                                                                       the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for contentities requires a license agreement (See http://www.isb-sib.ch/ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
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Yin W., Germiller J., Sanguineti C.,
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SMART; SM00032; CCP; 1.
SMART; SM00429; TCP; 1.
SMART; SM00539; NIDO; 1.
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01-FEB-1994
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01-FEB-1996 (Rel. 33, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 159.2 kDa protein K03H1.5 in chromosome
K03H1.5.
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Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., Mortimore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen is
Sims M., Smaldon N., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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MEDLINE=94150718; PubMed=7906398;
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                                                                                                                                                                         Hypothetical protein. SEQUENCE 1385 AA;
                                                                                                                                                                                                                                                                                                                              WormPep; K03H1.5; CE03459.
InterPro; IPR002909; IPT_TIG.
InterPro; IPR003886; Nidogen_ext.
InterPro; IPR000436; Sushi_SCR_CC
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 --CTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQ----HFDMAEP 108
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                                                                                                                                               the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an cmail to license@isb-sib.ch).
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                                              EMBL; M12069; AAA70191.1; -. EMBL; Z14092; CAA78474.1; -. PIR; S06434; S06434.
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Bonfleld J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hiller L., Jier M.,
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Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen R.,
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Therry-Mieg J., Thomas K., Vaudin M., Vaughan K.,
Waterston R., Watson A., Weinstock L., Wilkinson-Sproat J.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence up
01-MAR-2002 (Rel. 41, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "2.2 Mb of c
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MEDLINE-88334747; PubMed-3419531;
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LIN-12 OR R107.8.
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SIMILARITY: HIGH, TO C.ELEGANS GLP-1.
SIMILARITY: CONTAINS 13 EGF-LIKE DOMAINS.
SIMILARITY: CONTAINS 3 LIN/NOTCH REPEATS.
SIMILARITY: CONTAINS 5 ANK REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: LIN-12 IS INVOLVED IN SEVERAL CELL FATES DECISIONS REQUIRES CELL-CELL INTERACTIONS. IT IS POSSIBLE THAT LIN-12 ENCODES A MEMBRANE-BOUND RECEPTOR FOR A SIGNAL THAT ENABLES EXPRESSION OF THE VENTRAL UTERINE PRECURSOR CELL FATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mb of contiguous nucleotide sequence from chromosome III of
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Onor Katok	A;Reterence number: 214894; MULD:960Lb146 A;Accession: T10079 A;Status: preliminary; translated from GB/E A;Molecule type: mRNA A;Residues: 1-250 <shc> A;Cross-references: EMBL:030382; NID:g10408 A;Experimental source: cultivar Burpee Pick C;Genetics: A;Gene: EXP1 C;Function: mediates cell wall extension C;Superfamily: expansin F;1-23/Domain: signal sequence #status predicte F;24-250/Product: expansin #status predicte</shc>	RESULT 1 T10079 T10079 T20079	30 832 65.3 31 819.5 64.3 32 730 57.3 33 678 53.2 4 668 47.4 35 604 47.4 36 322.5 25.3 37 317 24.9 38 280 22.0 278 21.8 40 278 21.8 41 276 21.6 42 271 21.3 43 266.5 20.9 44 266.5 20.9 45 27.9
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2000	DDBJ PIDN:AAB37746.1; PID:g1040875 id <sig></sig>	i 16-Jul-1999 #text_change 21-Jul-2000 D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Shi i-9249, 1995 e analysis of expansinsa highly conserved, mu	expansin homolog Texpansin 3 - rice expansin 3 - rice expansin - upland hypothetical prote protein T12C24.10 expansin homolog Fexpansin (clone ppexpansin (clone ppexpansin (clone ppotta-expansin [impotta-expansin [impotein protein say beta-expansin - riprotein F1EC2.6 [impotobable beta-expansin - riprotable beta-expansin - riprotein F1EC2.6 [impotobable beta-expansin - riprotable beta-expansin - riprotable beta-expansin - riprotein F1EC2.6 [impotobable beta-expansin - riprotable - riprotable beta-expansin - riprotable beta-expan

expansin (clone pPtexp3) - loblolly pine (fragment)
c; Species: Pinus taeda (loblolly pine)
C; Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C; Accession: T09821
R; Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. RESULT T09821 δÃ Вb Ş В Вb ρ Q Matches 225; Query Match Best Local Similarity 204 181 144 121 N 84 19 24 1 DYGGWQSGHATFYGGGDASGTWGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 60 QNWQSNNYLNGQGLSFQYTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227 QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG 180 TCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGI 120 DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 83 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG TCTNDPKWCLPGTIRVTATNECPPNFALPNNNGGWCNPPLQHFDMAEPAFLQ1AQYRAGI 143 Conservative 99.2%; 99.1%; 2 Score 1265; DB 2; Pred. No. 3.9e-102; Mismatches 0 Length 250; Indels 0 Gaps 20 0

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T09826
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A; Accession: T09818
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C;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C;Accession: T09818
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A; Residues: 1-232 <HUT>
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A; Accession: T09821
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A;Description: Expansins are conserved in conifers and expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Description: Expansins are conserved in conifers and expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, July 1996
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                                                                                  NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQ 226
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                                                                                                                                                                                           CNDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIV
                                                                                                                                                                                                                      CTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIV 121
                                                                    NWQSNSYLNGQSLSFQVTTSDGRTIVSNNVAPSNWQFGQTFEGSQ
                                                                                                                             {\tt PILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVHAVSIKGSMSGWQPMSRNWGQ}
                                                                                                                                                                                                                                                      YGGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQ 181
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82.7%;
                                                                                                                                                                                                                                                                                                                                85.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P.B.; Diaz-Sala, C.; Greenwood, M.S.
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Pred. No. 3.4e-87;
                                                                                                                                                                                                                                                                                                                                Score 1087; DB 2; Pred. No. 9.1e-87;
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expansin (clone pPtexp5) - loblolly pine (fragment)
C;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C;Accession: T09826
R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Experimental source: clone pPtexp4 C; Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: mRNA
A;Residues: 1-232 <HUT>
A;Cross-references: EMBL:U64892; NID:g1778102; PID:g1778103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library, July 1996
A;Description: Expansins are conserved in conifers and expressed
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C;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: clone C; Superfamily: expansin
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A; Residues: 1-232 < HUT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQ
                                                                          PILYTRVPCLRKGGIRFTVNGHSCFNLVLITNVGGAGDVHAVSIKGPRSGWQPMSRNWGQ
                                                                                                 PVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQ 181
                                                                                                                                                                                                  CTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIV 321
                                                                                                                                                                                                                                                                            YGGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMQ 66
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                                                                                                                                                                           CNDDPQWCLPGTVTITATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIV 126
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82.2%;
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Pred. No. 6.7e-86;
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Pred. No. 1.
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A:Molecule type: mRNA
A:Residues: 1-246 <CHO>
A:Cross-references: EMBL:U85246; NID:g1815680; PIDN:AAB81662.1; PID:g1815681
                                                                                                                                                                                                                                                                                                                              C;Accession: T04175
R;Cho, H.T.; Kende, H.
R;Cho, H.T.; Kende, H.
Plant Cell 9, 1661-1671, 1997
A;Title: Expression of expansin genes is correlated with
A;Reference number: Z15042; MUID:97480100
A;Accession: T04175
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                                                                                                                                                                                                                                                                                                                                                                                                                                   expansin - rice
C:Species: Oryza sativa (rice)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 26-May-2000
C:Accession: T04175
                8
                                                                                                                                                                     C; Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Map position:
C; Superfamily.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Gene: At2g40610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable expansin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: F84831
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: GB:AE002093; NID:g2651297; PIDN:AAB87577.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-253 <STO>
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                                                                                                                                  Query Match
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                21
                                                                                                                 Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Match 84.1%; score 1072.5; DB Local Similarity 82.9%; Pred. No. 1.8e-85
                                                                                                                                                                                                 EXP4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 60
      YGGWQSAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGAACGSCYELR 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GONWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KCNDDPRWCLGSTITVTATNFCPPNPGLSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGI 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   189;
                                                                                                                 Similarity
                                                                                          Conservative
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                                                                                                           81.6%;
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                                                                                                        Score 1041; DB 2;
Pred. No. 9.3e-83;
                                                                                        Mismatches
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                                                                                                                             Length 246;
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A; Experimental source: cultivar Siokra 1-2 C; Genetics:
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C;Accession: T09786
R;Orford, S.J.; Timmis, J.N.
Biochim. Biophys. Acta 1398, 342-6, 1998
A;Title: Specific expression of an expansin gene
A;Reference number: Z14468; MUID:9655931
A;Accession: T09786
A;Cross-references: EMBL:AF043284; NID:g2811277; PID:g2811278
                                A; Molecule type: mRNA
A; Residues: 1-258 < ORF>
                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                      C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                         expansin - upland cotton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: induces extension (creep) in plant cell C; Superfamily: expansin \ensuremath{\mathsf{C}}
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R;Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Muson, S.J.; Shi Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A;Title: Molecular cloning and sequence analysis of expansins-a highly conserved, mu
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T03298
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A; Residues: 1-251 <SHC>
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C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
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A;Accession: T03298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNWQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFXQTFEGGQF 251
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RCDNDGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGI 144
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78.9%;
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A; Description: C; Superfamily:
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C; Function:
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 02-Sep-2000
C;Accession: T50554
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A;Title: Molecular cloning and sequence analysis of expansins—a highly conserved, multi
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A; Gene: EXP1
expansin EXP2 [imported] - C;Species: Arabidopsis thal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: EMBL:U30476; PIDN:AAB38070.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-237 <SH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Accession: T50654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: Z14894; MUID: 96016146
                                                    T50656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                152 VPVMFRRVSCVKKGGIRYTMNGHSYFNMVLITKLGGAGDITSVSIKGSRTGWLPMSRNWG 211
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      121
                                                                                                                                192
                                                                                                                                                                  183 WQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQ 226
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RCNNDPQWCISRTITVTATNFCPPNYALSSDNGGWCNPPREHFDLAEPRFLRIAEYRAGI 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNGGWQTAHATFYGGADATGTMGGACGYGNLYSQGYGTSTAALSTALFNNGLSCGACYEL 91
                                                                                                                                                                                                           VSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQN 182
                                                                                                                                                                                                                                                                                    QNDGKWCLPGSIVVTATNECPPNNALPNNAGGWCNPPQQHEDLSQPVFQRIAQYRAGIVP
                                                                                                                                                                                                                                                                                                                                                                                                     GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC 62
                                                                                                                              WOSNSYLNGQSLSFKYTTSDGQTIVSNNVANAGWSFGQTFTGAQ 235
                                                                                                                                                                                                                                                                                                                           INDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIVP 122
                                                                                                                                                                                                                                                                                                                                                                GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                           176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1-237 <SHC>
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
              d] - Arabidopsis thal
thaliana (mouse-ear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              80.5%; Score 1027; DB 2; 78.6%; Pred. No. 1.4e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26;
                                                                                                                                                                                                                                                                                                                                                                                                                                             24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1041; DB 2;
Pred. No. 9.8e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                    thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 24; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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C;Accession: T50656
R;Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Sproc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A;Title: Molecular cloning and sequence analysis of expansins--a highly conserved, A;Reference number: Z14894; MUID:96016146
A;Accession: T50656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
C;Accession: T50656
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Description: induces of C; Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: EMBL: U30481; PIDN: AAB38073.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: mRNA
A; Residues: 1-255 <SHC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable expansin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
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                                                                                                                                                                                                                                                                       A; Map position:
C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-248 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Accession: C84444
В
                                                                                                                                                                                                                                                                                                               A; Gene: At2g03090
                                                                                                                                                                                                                                                                                                                                           C; Genetics:
                                                                                                                                                                                                                                                                                                                                                              A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                    Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             121 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTG-WQSMSRNW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
64 NDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIVPV 123
                                                                                          24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 60
                                                                                                             4 GWOSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMYCT 63
                                                                                       GWVNAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIKCQ 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCEDDPEWCIPGSIIVSATNFCPPNFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGI 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VPVAFRRVPCEKGGGTRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW
                                                                                                                                                                                    174;
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178; Conserv
                                                                                                                                                                                                                                                                       expansin
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                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                 GB:AE002093; NID:g3461833; PIDN:AAC32927.1; GSPDB:GN00139
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                                                                                                                                                                                                    79.9%; Score 1019; DB 2; 77.7%; Pred. No. 7.5e-81;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26; Mismatches
                                                                                                                                                                                    24; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23;
                                                                                                                                                                                                                                 Length 248;
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Gaps

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A:Map position: 3
A:Introns: 52/1; 1
A:Note: T22E16.160
                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-260 <BEN>
A; Cross-references: EMBI
                                                                                                                                                                                                                                                                                                 C;Accession: T47689
R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer,
                                                                                                                                                                                                                                                                                                                                                    expansin-like protein - Arabidopsis thaliana
N;Altornate names: protein T22E16.160
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
                                                                                                                  C; Genetics:
                                                                                                                       A; Experimental source: cultivar Columbia; BAC clone T22E16
                                                                                                                                                                                                                                                      A; Reference number: Z24472
A; Accession: T47689
                                                                                                                                                                                                                            A; Status: preliminary
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A:Map position: 2
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A; Residues: 1-257 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       209 QNWQSNAVLVGQALSFRVTGSDRRTSTSWNMVPSNWQFGQTFVGKNF 255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              149 VPVSYRRVPCRKRGGIRFTINGHRYFNLVLITNVAGAGDIVRASVKGSRTGWMSLSRNWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              121 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89 ANDPOWCHSGSPSILITATNFCPPNLAQPSDNGGWCNPPREHFDLAMPVFLKIAQYRAGI 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 TNDPKWCLPG--TIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29 GAWQNAHATEYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALENNGMSCGACFELKC 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                204 QSNNLLNGQALSFKVTASDGRTVVSNNIAPASWSFGQTFTGRQF 247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           184 QSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         144 SYRRVPCMRRGGIRFTINGHSYENLVLVTNVGGAGDVHSVAVKGSRTRWQQMSRNWGQNW 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                124 SFRRVPCMKKGGVRFTINGHSYFNLVL1TNVGGAGDVHSVSIKGSRTGWQSMSRNWGQNW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GGWOSGHATFYGGGDASGTMGGACGYGNLYSOGYGTNTVALSTALFNNGLSCGACFEMTC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                        EMBL: AL132975
                                                                                                                                                                                                                                                                                            Sequence Database,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.3%; Score 985; DB 2; Length 257; 75.8%; Pred. No. 6.8e-78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: GB:AE002093; NID:g3236246; PIDN:AAC23634.1; GSPDB:GN00139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Residues: 1-262 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Reference number: A84420; MUID: 20083487
A; Accession: C84795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thallana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Map position: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: At2g37640; F13M22.14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A:Cross-references: EMBL:AC004684; NID:g3236234; PID:g3236246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Status: translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, K.C.; Syke submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Reference number: Z14677
A; Accession: T02530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probable expansin F13M22.14 - Arabidopsis thaliana ("Species: Arabidopsis thaliana (mouse-ear cress) ("C;Date: 05-Mar-1999 #text_change 16-Feb-200)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A: Experimental source: cultivar Columbia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Residues: 1-262 < ROU>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
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181 QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
                                                154 VPVSYRRVPCRKIGGIRFTVNGFRYFNLVLVTNVAGAGDINGVSVKGSKTDWVRMSRNWG
                                                                       121 VPVSFRRVPCMKKGGVRFTINGHSYENLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWG
                                                                                                                                           94 TDDDRWCVPGNPSILVTATNFCPPNFAQPSDDGGWCNPPREHFDLAMPMFLKIGLYRAGI 153
                                                                                                                                                                                    63 TNDPKWCLPG--TIRVTATNPCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGI 120
                                                                                                                                                                                                                                         34 GPWQNAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGFSCGACFEIKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        212 QNWQSNAVLVGQSLSFRVTSSDRRTSTSWNIAPSNWQFGQTFVGKNF 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 VPISYRRVACRKSGGIRFTINGHRYENLVLITNVAGAGDIARTSVKGSKTGWMSLTRNWG
                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSKTGWOSMSRNWG 180
                                                                                                                                                                                                                                                                     3 GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 VNDPKWCHPGNPSVFVTATNFCPPNLAQPSDNGGWCNPPRSHFDLAMPVFLKIAEYRAGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 THDPKWCLPG--TIRVTATHFCPPNFALPHDDGGWCNPPLQHFDMAEPAFLQIAQYRAGI 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32 GSWQTAHATFYGGNDASGTMGGACGYGNLYSQGYGTNTAALSTSLFNSGOSCGACFEIKC 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC 62
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                                                                                                                                                                                                                                                                                                                                                      165;
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                                                                                                                                                                                                                                                                                                                                       74.8%; Score 954; DB 2; Length 262; 72.7%; Pred. No. 3.3e-75; Indels
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73.1%; Pred. No. 1e-75;
ative 24; Mismatches
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Search completed: October 11, 2002, 15:01:01 Job time: 11.3919 secs

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Maximum DB seq
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      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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2: /cgn2_6/ptodata/2,

3: /cgn2_6/ptodata/2,

4: /cgn2_6/ptodata/2,

5: /cgn2_6/ptodata/2,

6: /cgn2_6/ptodata/2,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cgn2_6/ptodata/2/1aa/5A_COMB.pep:*
/cgn2_6/ptodata/2/1aa/5B_COMB.pep:*
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/cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep:*
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US-09-092-160-5
US-09-092-160-3
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.81 QNWQSNNYLNGQGLSFQYTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227	1 VPVSFRRVPCMKKGGVRFTINGHSYENLVLITNVGGAGDVHSVSIKGSRTGWQ: 	61 TCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQTAQY 	1 DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCG. 	Match 100.0%; Score 1275; DB 4; Length 227; Local Similarity 100.0%; Pred. No. 2e-118; les 227; Conservative 0; Mismatches 0; Indels 0	LENGTH: 227 TYPE: PRT ORGANISM: Artificial Sequence FEATURE: OTHER INFORMATION: Description of Artificial Sequence: cucumbe OTHER INFORMATION: expansin S-09-092-160-7	05-12	05-12 1: 08/242,09	ENT APPLICATION NUMBER: US/09/092,160C ENT FILING DATE: 1998-06-05 IER APPLICATION NUMBER: 08/440.517	ICANT: Sh1, Jun E OF INVENTION: PURIFIED EXPANSIN PROTEINS REFERENCE: 1194/1C114US3	ICANT: MCQueen-Mason, Simon ICANT: Guiltinan, Mark J ICANT: Shcherban, Tatyana	- 3	ALIGNMENTS	9 6.2 402 1 US-08-325-630-11 5 6.2 418 4 US-09-254-733-5	5 6.4 402 2 US-08-491-988-9 9 6.2 402 1 US-08-460-806-11	5 6.6 633 3 US-09-041-991A-10	95.5 7.5 145 4 US-08-441-507-1 93.5 7.3 145 4 US-08-441-507-2	19.5 9.4 145 4 05-00-433-280-4 19.5 9.4 145 4 05-08-174-739-4 00.5 7.9 54 3 US-08-1750-419A-12	5 9.4 145 4 US-08-413-974-4 9.4 145 4 US-08-434-418-4	173 13.6 200 4 US-08-441-507-5 173 13.6 200 4 US-08-441-507-4 39.5 10.9 122 4 US-08-441-507-23	4 16.0 245 4 US-08-441-507-24
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181 QNWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227

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APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guittinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
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US-08-440-517A-6
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                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                      Sequence 6, Application US/09092160C Patent No. 6255466
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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TYPE: AMINO ACID
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                                                                                                                                                                                                                                                                                                                                          VPVSYRRVPCVKKGGIRETINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWG
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SHCHERBAN, TATYANA;
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78.0%;
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SEQ ID NO 6
LENGTH: 226
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GENERAL INFORMATION:
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Best Local Similarity
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EARLIER APPLICATION NUMBER: 08/C
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/C
                                                                                                                   CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
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CORRESPONDENCE ADDRESS:
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SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
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APPLICANT: GUILTINAN, MARK;
                                                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
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                                                                                                                                                        FILING DATE:
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                                                                                  LENGTH:
                                                                                                                                                                       APPLICATION NUMBER:
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5, 5959082
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                                                                AMINO ACID
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SHCHERBAN, TATYANA;
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80.1%;
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Score 1021;
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Length 228;
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 US-09-092-160-2
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CURRENT APPLICATION NUMBER: US/09/092,16(
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/40,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID NO 2
LENGTH: 228
TYPE: PRT
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Matches 175; Conserv
                                                                                                                                                                                                                                                                                                               Query Match
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APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
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OTHER INFORMATION: Description of Artificial Sequence: rice expansin
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                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                           3 GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEG 224
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  QNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVP
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                WQSNNYLNGQGLSEQVTLSDGRTLTAYNLVPSNWQFGQTYEG 224
                                                                   VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN 182
                                                                                    VSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQN 182
                                                                                                                                                                                                          WQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTG 224
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                                                                                                                                                                                                                                                                              80.1%; Score 1021; DB 4; 78.8%; Pred. No. 2.6e-93; tive 23; Mismatches 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         US/09/092,160C
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3; Mismatches 24
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                                                                                                                                                                                                                                                                                                                Length 228;
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US-08-440-517A-5
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APPLICANT: COSCROV
APPLICANT: GUILTIN
APPLICANT: SHCHERB
APPLICANT: SHI, JU
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                                                                                                                                                                                                                                                                                     Best Local Si
Matches 171;
                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
118 VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW
                                                                                                       121 VPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTG-WQSMSRNW 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: NEC 281
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                           TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY:
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                                                                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                               1 DNGGWERGHATFYGGADASGTMGGACGYGNLHSOGYGLQTAALSTALFNSGQKCGACFEL 60
                                                                                                                                                                                                                                  1 DYGGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEM 60
                                                                                                                                            TCEDDPEWCIPGSIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGI 117
                                                                                                                                                              TCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGI 12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                     75.5%; Score 962; DB 2; Length 225; 75.0%; Pred. No. 1.7e-87; ative 26; Mismatches 27; Indels
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GENERAL INFORMATION:
APPLICANT: COSGROVE, Daniel J
APPLICANT: McQueen Mason, Simon
APPLICANT: Gulltinan, Mark J
APPLICANT: Shih, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517

US-09-092-160-5

Sequence 5, Application US/09092160C Patent No. 6255466

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US-08-440-517A-3
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Query Match
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GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1 SEQ ID NO 5
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                                                                                                                                    CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
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                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE
ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
                                                                                                                     SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                              SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
APPLICANT: SHCHERBAN, TATYANA;
APPLICANT: SHI, JUN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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                                                                     TOPOLOGY:
                                                                                      TYPE:
                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                    COMPUTER:
                                                                                                   LENGTH:
                                                                                                                                                                                         APPLICATION NUMBER: US/08/440,517A
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16802-7000
                                                                                    AMINO ACID
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75.0%; Pred. No. 1.7e-87;
tive 26; Mismatches 27
             67.3%;
             Score 857.5;
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CURRENT APPLICATION NUMBER: U$/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION UMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
EARLIER FILING DATE: 1993-05-12
VOLUMBER: DESCRIPTION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
SOFTWARE: PATENTIN VOR: 7
SOFTWARE: PATENTIN VOR: 7
SOFTWARE: PATENTIN VOR: 2.1
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; OTHER INFORMATION: Xaa is unknown or other.
US-09-092-160-3
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APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
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175
                        182 NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
                                                                                        115 PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       175 NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               122 PVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQ 181
                                                                                                                                                                                      63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 114
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                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 TNDPKWCLPG-TIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIV 121
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                                                                                                                   PVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQ 181
                                                                                                                                                                                                                 TNDPKWCLPG-TIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIV 121
                                                                                                                                                                                                                                                                                 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC 62
NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 220
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                                                                                                                                                                                                                                                                                                                                                                         Score 857.5; DB 4;
Pred. No. 3.6e-77;
6; Mismatches 39;
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                                                                                                                                                                                                                                                                                                                                                                                                                        Length 222;
                                                                                                                                                                                                                                                                                                                                                                              Indels
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CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 225
TYPE: PRT
ORGANISM: Lycopersicon esculentum cv. T5
US-09-362-642-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       sequence 2, Application US/08845539 Patent No. 5929303
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Patent No. 6350935
GENERAL INFORMATION:
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Best Local 9
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APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                      APPLICATION NUMBER: US/08
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bastlan, Kevin L.
                                                                                                                                     SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     119 GIVPVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWOSMSRN 178
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                                                                                                                                                                                                                                                                                                                                      STREET: TWO EMBARCAC
CITY: San Francisco
           REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                             STATE: California
                                                                                                                                                                                                                                                                                                            COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           / Match 65.8%; Score 839; DB 4; Local Similarity 74.7%; Pred. No. 2.4e-75; nes 145; Conservative 21; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3 GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFENTC 62
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                                                                                                                                                                                                                                                                                    94111-3834
AGENT AND BASTIAN, Kevin L.
Bastian, Kevin L.
34,774
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                                                                                                                                                                                                                                                                                                            USA
                                                                                                                         US/08/845,539
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US-08-845-539-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 145;
                                                                                        TELEFAX: (415) 576-0300 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                           NAME: Bastian, Kevin L. 774
REGISTRATION NUMBER: 34,774
REFERRUGE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                  MOLECULE TYPE:
                                                                                                                                                                                                                                       FILING DATE: 25-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM FC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 023070-078200US TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: (
                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211 WGQNWQSNAVLTGQ 224
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                                                   TYPE: amino acid
                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET:
                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                              94111-3834
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                                                                 179 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 USA
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              protein
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                                                                                                                                                                                                                                                                                                       US/08/845,539
                                                                                                              6:
                                                                                                                                                                                        023070-078200US
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US-08-440-517A-4
                                                                                                                                                                                                                                                                                                                                                                 Дb
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US-09-362-642-6
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LENGTH: 179
TYPE: PRT
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patent No. 6350935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 62.5%; Score 797; DB 4; Length 179; Best Local Similarity 79.1%; Pred. No. 2.6e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
TITLE OF INVENTION: to Control Fruit Texture and Softening
TILE REFERENCE: 023070-078210US
CURRENT FILING DATE: 1999-07-27
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                              Sequence 4, Applic Patent No. 5959082
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                 APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
APPLICANT: SHCHERBAN, TATYANA;
APPLICANT: SHI, JUN
                                                                                          APPLICANT: SHI, JUN
TITLE OF INVENTION: PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   123 VPCRKQGGIRFTINGFRYFNLVLITNVAGAGDIVRVSVKGSNTGWMSMSRNWGQNWQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     128 VPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQNWQ 184
                                                                                                                                                                                                                                                                                                                                                                                   128 VPCMKKGGVRFTINGHSVENLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQNWQ 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10 ATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTCTNDPKWC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 HPGSPCIFITATNFCPPNFALPNDNGGWCNLPRTHFDLAMPMFLKIAEYRAGIGPVSYRR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70 LPGT--IRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIVPVSFRR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                            10 ATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTCTNDPKWC 69
              ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY STREET: 113 TECHNOLOGY CENTER CITY: UNIVERSITY PARK
STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 ATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTAFFNNGLSCGACFEIKCANDPRWC 62
                                                                                                                                                                                                                                                                                                                                                                 140;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/09362642
                                                                                                                                                                                                                                                                    Application US/08440517A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bennett, Alan B
PENNSYLVANIA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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US-09-092-160-4
                                                                                                                                                                                                                                                                        CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1993-05-12
EARLIER FILING DATE: 1993-05-12
NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER: 0F SEQ. ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; GENERAL INFORMATION:
US-09-092-160-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 137; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 4, Application US/09092160C Patent No. 6255466
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                    SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Shcherban, Tatyana APPLICANT: Shi, Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Guiltinan, Mark J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: McQueen-Mason, Simon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS FILE REFERENCE: 1194/1C114US3
                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                        NAME/KEY: UNSURE LOCATION: (2)..(227)
                                                                                                     OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis OTHER INFORMATION: expansin
                                                                                                                                                                       ORGANISM: Artificial Sequence
                                                                                                                                                                                         TYPE: PRT
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                    OTHER INFORMATION: Xaa is unknown or other
                                                                                   FEATURE:
                                                                                                                                                FEATURE:
                                                                                                                                                                                                           LENGTH: 227
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         186 WQSNAYLAGQSLSFTVQLDDGRKVTAWNXAPXNW 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      183 WQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNW 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 VNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGAN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 VSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                66 QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         65 DPKWCLPG--TIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIVP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Match 60.2%; Score 767.5; DB 2; Length 227; Local Similarity 64.0%; Pred. No. 2.9e-68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        6 QSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC-TN 64
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Post-processing: Minimum Match 0%
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                                                                                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A_Geneseq_032802:*
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SUMMARIES
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AAG299	AAG51	AAG15	AAG51	AAG15	AAG36	AAG09	AAG09	AAG09	AAE00	AAG30	AAG30	AAG29	AAG29	AAG36	AAG36	AAG36	AAR94	AAG05	AAG05		AAG46		21 AAG36445										AAG516	
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AAR94527
                       Expansin proteins which alter the mechanical strength of poly:saccharide(s) - useful in paper mfr. and recycling
                                                                                                                                                                            WPI; 1996-201150/21
N-PSDB; AAT13320.
                                                                                                                                                                                                                                                                                                             Cosgrove DJ, McQueen-Mason S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-MAY-1995;
12-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expansin-29; plant cell wall; cellulose; paper recycling; de-inking;
                                                                                                                                                                                                                                                                                                                                                                                                   (PENN-) PENN STATE RES FOUND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          04-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AU9540262-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      polysaccharide; cucumber.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cucumber expansin-29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        08-JUL-1996 (first entry)
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93US-0060944.
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QΥ
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AAG25443
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25-FEB-1999

05-MAR-1999

09-MAR-1999

23-MAR-1999

23-MAR-1999

25-MAR-1999

01-APR-1999

01-APR-1999

06-APR-1999

16-APR-1999

16-APR-1999

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                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                  Protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana protein fragment SEQ ID NO: 29510
                                                                                                                                                                                                                                               25-FEB-2000;
                                                                                                                                                                                                                                                                              06-SEP-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 30; 60pp; English.
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   99US-0126264.
99US-0127462.
99US-0127462.
99US-0128234.
99US-0128714.
99US-0128715.
99US-0130077.
99US-0130449.
99US-0130891.
99US-0131449.
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99US-0123180.
99US-0123548.
99US-0125788.
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99.1%;
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11-MAY-1999
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06-JUL-1999;
08-JUL-1999;
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18-JUN-1999
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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12-JUL-1999;
13-JUL-1999;
           20-JUL-1999;
20-JUL-1999;
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21-JUL-1999;
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19-JUL-1999;
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16-JUL-1999;
19-JUL-1999;
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15-JUL-1999;
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19-JUL-1999;
           990S-0132663

990S-0134268

990S-0134218

990S-013421

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990S-013523

990S-013522

990S-0135621

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99US-0132407.
99US-0132484.
99US-0132485.
99US-0132486.
99US-0132487.
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21-JUL-1999; 21-JUL-1999; 22-JUL-1999; 22-JUL-1999;

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  25-PEB-1999

05-MAR-1999

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23-MAR-1999

25-MAR-1999

29-MAR-1999

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16-APR-1999
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29-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                        Protein identification; signal transduction pathway; metabolic parhway; hybridisation assay; genetic mapping; gene expression control; promotor; termination sequence.
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                                                                                                                                                                                                                                                                                                  EP1033405-A2.
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|||||||:::||||||:|||
GONWQSNSYMNDQSLSEQVTTSDGRTLVSNDVAPSNWQFGQTVQGGQF 253
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89; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first
99US-0121825
99US-0123180
99US-0125788
99US-0125788
99US-0126785
99US-0127462
99US-0127462
99US-012824
99US-0128714
99US-0129845
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99US-0160980

99US-0161404

99US-0161404

99US-0161405

99US-0161405

99US-0161359

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99US-0161922
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82.98;
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Pred. No. 3.7e-100;
17; Mismatches 21;
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RESULT 4
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Matches 189;
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05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
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                                                                                            25-FEB-2000;
                                                                                                                        06-SEP-2000.
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                                                                                                                                                                                                      Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter termination sequence.
                                                                                                                                                                                                                                                                                                                                              AAG06546 standard; Protein;
                                                                                                                                                                            Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                            17-OCT-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GONWQSNNYLNGGGLSFQVTLSDGRTLTAYNLVPSNWQFGGTYEGPQF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TCTNDPKWCLPGTIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGI 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KCNDDPRWCLGSTITVTATNFCPPNPGLSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGI
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39; Conservative
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                                                                                                                                                                                                                                                                                                                                               241
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                                                                                                                                                                                                                 promoter;
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07-MAY-1999;
11-MAY-1999;
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14-MAY-1999;
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30-APR-1999
04-MAY-1999
05-MAY-1999
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14-MAY-1999;
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RESULT 5
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                                                                                          Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                                                                                                      Arabidopsis thaliana protein fragment SEQ ID NO: 65551.
                            06-SEP-2000.
                                                                                    termination sequence.
                                                                                                                                            18-OCT-2000 (first entry)
                                                                                                                                                                                AAG51633 standard;
         25-FEB-2000; 2000EP-0301439
                                               EP1033405-A2
                                                                Arabidopsis thaliana
                                                                                                                                                                                                                              196
                                                                                                                                                                                                                                                183
                                                                                                                                                                                                                                                                   136
                                                                                                                                                                                                                                                                                     123
                                                                                                                                                                                                                                                                                                                                          63 TNDPKWCLPGTIRVTATNECPDNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIVP 122
                                                                                                                                                                                                                                                                                                        76
                                                                                                                                                                                                                                                                                                                                                                                                      Match
                                                                                                                                                                                                                            VSERRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQN 182
                                                                                                                                                                                                                                                                                                        ENDGKWCLPGSIVVTATNFCPPNNALANNNGGWCNPPLEHFDLAQPVFQRIAQYRAGIVP
                                                                                                                                                                                                                                                                   VSYRRVPCRRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAAIKGSRTVWQAMSRNWGQN
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78.7%; Pred. No. 5.5e-96;
vative 25; Mismatches 23
                                                                                                                                                                                 Protein; 241
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                                                                                                                                                                                                                                                                                                                                                                                                        DB 21;
                                                                                                                                                                                                                                                                                                                                                                                      23;
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                                                                                                                                                                                                                                                                                                                                                                                                          241;
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promoter;
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13-OCT-1999;
13-OCT-1999;
                                                                     protein identification; signal transduction pathway; metabolic pathway;
hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 65570.
                                                                                                                                                                                                          AAG51647 standard; Protein; 241 AA
                            Arabidopsis thaliana.
                                                          termination sequence.
                                                                                                                                                 18-OCT-2000 (first entry)
                                                                                                                                                                                                                                                                                 Similarity
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990S-0157753.
990S-0157865.
990S-0158029.
990S-0158232.
990S-0158369.
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99US-0159741.
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99US-0159329.
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99US-0159637.
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pred. No. 5.5e-96;
5; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 241;
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           25-FEB-1999
05-MAR-1999
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06-APR-1999
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01-JUL-1999
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                                     99US-0126785.
99US-0127462.
99US-0128714.
99US-0130479.
99US-0130077.
99US-0132408.
99US-0132486.
99US-0132486.
99US-0134221.
99US-013422.
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99US-013428.
99US-013945.
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99US-0126264.
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EP1033405-A2

14-JUL-1999; 15-JUL-1999; 16-JUL-1999;

16-JUL-1999

08-JUL-1999; 09-JUL-1999; 12-JUL-1999; 13-JUL-1999; 02-JUL-1999; 06-JUL-1999; 08-JUL-1999;

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99US-0142055

99US-0142900

99US-0142907

99US-0144086

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99US-0144331

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99US-0145086

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99US-0145218

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Best Local
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                                Arabidopsis thaliana protein fragment SEQ ID NO: 3356.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                         17-OCT-2000
                                                                              AAG06545;
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07-OCT-1999
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12-OCT-1999;
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                                                       (first entry)
                                                                                                                                                                                                                                                                                                                    Conservative
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99US-01556458
99US-01556596
99US-0157717
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99US-0158023
99US-0158232
99US-0159294
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99US-0160767
99US-0160981
99US-0161406
99US-0161369
99US-0161369
99US-0161369
99US-0161369
                                                                                                 Protein; 249
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; Pred. No. 5.5e-96;
25; Mismatches 23;
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                                                                                                                                                                                                                                                                                                                                   Length 241;
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990S-0151066.
990S-0151080.
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9463. 9750. 9763. 9817. 9817. 9899. 0353.	9459. 9460. 9461. 9462.	9456. 9457. 9458.	9492. 9454. 9455.	9452.	3847. 9119.	7724. 3094.	7528. 7502.	782.	392.	629.	124.	768. 941	221. 370.	218. 219.	256.	487.	485.	407.	048.	891.	449. 510.	077.	714.	162.	785.	264	48	325. 180.	139.				
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 (first entry)
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990S-015378

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Pred. No. 5.7e
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al Similarity
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milarity 78.7%;
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                                80.9%;
                    25;
                  Score 1031; DB 21; Length pred. No. 6.7e-96; Fig. Mismatches 23; Indels
                                                            280;
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                                          Query Match
Best Local :
                              Matches
                                                                                                   Expansins are a novel class of proteins that catalyse the extension of plant cell walls and the weakening of the hydrogen bonds in pure cellulose. 2 Expansins (AAR94528 and AAR94529) have been identified rice and 3 in Arabidopsis (AAR94530-32). A cDNA clone (AAR13320) coding for cucumber expansin 29 (AAR94527) has been obtd. Expansins can be used e.g. in the mfr., de-inking and recycling of paper, in the textile industry, to aid delignification processes, to alter gel
                                                                          Sequence
                                                                                                                                                                                                                   Expansin proteins which alter the mechanical strength of poly:saccharide(s) • useful in paper mfr. and recycling
                                                                                                                                                                                                  Disclosure; Page 30-31; 60pp; English.
                                                                                                                                                                                                                                                            WPI; 1996-201150/21.
                                                                                             mechanical strength,
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12-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
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3 GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGWOSGHATFYGGGDASGTMGGACGYGNLYSOGYGTNTVALSTALENNGLSCGACFEMTC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQN 182
                             175;
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                                      Similarity
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                            Conservative
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                                     80.1%;
                         Score 1021; DB 17;
Pred. No. 5.2e-95;
Pred. Mismatches 24;
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RESULT 14
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05-MAR-1999;
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                                                                                                                                                                                                                                                                                                                                                    06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                         Protein identification; signal transduction
                                                                                                                                                                                                                                                                                                                                                                                                                                           Arabidopsis thaliana protein fragment SEQ ID NO: 27311.
                                                                                                                                                                                                                                                                                                                                                                                                          termination sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                    hybridisation assay;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QNDGKWCLPGSIVYTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVP
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990S-0125788

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                                                                                                                                                                                                                                                                                                                                                                                                                  genetic
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                                                                                                                                                                                                                                                                                                                                           termination sequence.
                                                                                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                                                                                                                                         Arabidopsis thaliana protein fragment SEQ ID NO: 54163.
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26-OCT-1999
99US-0146388.
99US-0147038.
99US-0147204.
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99US-0147303.
99US-0147416.
99US-0147416.
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99US-0148319.
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Matches 174; Conservative
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29-OCT-1999;
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                        184 OSNNYLNGQGLSFQYTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
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207 OSNNLLNGQALSFKYTASDGRTVVSNNIAPASWSFGQTFTGRQF 250
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99US-0161992.
99US-0161993.
99US-0162142.
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2002, 14:56:45
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24; Mismatches 26;
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Search completed: October 11, Job time: 26.1292 secs

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CATJ_MOUSE
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16-CCT-2001 (Rel. 40, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
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                                                                                                                DISULFID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-C57BL/6; TISSUE-Placenta;
Sol-Church K., Frenck J., Troeber D., Mason R.W.;
"Cloning of a mouse cysteine protease.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
-!- SUBCELLULAR LOCATION: Lysosomal (Potential).
-!- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA.
-!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE PAPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                        CHAIN
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                                                                                                                                                                                                                                                                                                                        Hydrolase; Thiol
                                                                                                                                                                                                                                                                                                                                                                    PROSITE; PS00139; PROSITE; PS00639;
                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PR00705;
                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000668; Peptidase_C1
InterPro; IPR000169; Thiolprot_act
Pfam; PF00112; Peptidase_C1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Tisljar K., Deussing J., Peters C.;
"Cathepsin J. a novel murine cysteine protease of the papain family
with a placenta-restricted expression.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-C57BL/6J; TISSUE-Embryo; MEDLINE-99456833; PubMed-10526153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       131 YHFDI 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MGI:1349426; Ctsj
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P07711;
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                                                                                                                                                                                                                                                                                                                        protease;
                                                                                                                                                                                                                                                                                                                                                                                                                  PAPAIN.
                                                                                                                                                                                                                                                                                                                                                                                        THIOL_PROTEASE_CYS; 1.
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                                               LYMPHOCYTE EFFECTOR FUNCTION.

-! CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Xbb-(-XCC, except when Xaa is Arg or Lys, or Xbb or XCC is Pro.
-!- SUBUNIT: DIMER OF AN ALPHA CHAIN AND A BETA CHAIN CROSS-LINKED BY A DISULFIDE BOND.
-!- SUBCELLULAR LOCATION: Lysosomal.
-!- TISSUE SPECIFICITY: BROADLY DISTRIBUTED, BUT HIGHER LEVELS FOUND
                                                                                                                                                                 McGuire M.J., Lipsky P.E., Francisco N.M.C., Thiele D.L.;
Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: THIOL PROTEASE. HAS DIPEPTIDILEPTIDISE ACT
                                                                                                                                                                                                                                                            MCGuire M.J., Lipsky P.E., Thiele D.L.;
"Cloning and characterization of the cDNA encoding mouse dipeptidyL
                                                                                                                                                                                                                       STRAIN-BALB/C;
                                                                                                                                                                                                                                         REVISIONS
                                                                                                                                                                                                                                                                                                                        MEDLINE-97276897; PubMed-9130590;
                                                                                                                                                                                                                                                                                                                                                                                murine dipeptidyl peptidase I.";
J. Biol. Chem. 272:10695-10703(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P97821; 008853;
15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Dipeptidyl-peptidase I procursor (EC 3.4.14.1) (DPP-I) (Cathepsin C) (Cathepsin J) (Dipeptidyl transferase).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         _MOUSE
                                                                                                                                                                                                                                                                                                                                               STRAIN-BALB/C;
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-97256790; PubMed-9099719;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-129/SVJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                          "Molecular cloning, chromosomal localization, and expression of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATC_MOUSE
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              296 LIKNSWGEEWGMNGYMQ 312
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              247 AIDASHDSFRFY----NGGIYYEPNCSSYFVNHAVLVVGYGSEGDVK-----DGNNYW-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 A-----FRRVPCEKGGGIRFTINGNPYF--DLVLITNVGGAGDIRAVSLKGSKTDOWQ 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       204 EGKDGP------CRYRSEN-ASANITDYVNLPP-----NELYLWYAVASIGPŸSA 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 152 WKTGNLTPLSVQNLLDCSKTVGNKGCQSGTAHQ-----AFEYVLKNKGLEAEATYPY 203
    SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE
   PAPAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 TCEDDPEWCIPGSIIVRYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVPV 120
                               AND BRAIN.
                                              IN LUNG,
                                                                                                                                                  DEGRADE GLUCAGON. PLAYS A ROLE IN THE GENERATION OF CYTOTOXIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                T.N., Armstrong R.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
FAMILY OF THIOL
                                       LIVER, KIDNEY AND SPLEEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               333 AA;
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37147 MW;
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PROTEASES
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; F9A8FF1D5A13B721 CRC64;
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                                      LOWER LEVELS
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                                    IN TESTIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning, expression and immunological characterization of Ory s 1, the major allergen of rice pollen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=96069591; PubMed=7590339;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- DISEASE: CAUSES GRASS POLLEN ALLERGY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- TISSUE SPECIFICITY: EXPRESSED IN MATURE ANTHERS BUT NOT VEGETATIVE OR OTHER FLORAL TISSUES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE=Anther
                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000882; Pollen_allergen. pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; U31771; AAA86533.1; -. HSSP; P43214; 1WHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                            CHAIN
                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                   Allergen; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50843; EXPANSIN_CBD; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                  proDom; pD002179; Pollen_allergen; 1.
191 SLSFQVTDSDGRTVVSYDVVP 211
                                169
                                                                                                                       83 FALANDNGGWCNPPLK--HFDLAEPAFLQIAQ----YRAGIVPVAFRRVPCEKGGGIRFT 136
                                                                                                                                                       61
                                                                                                                                                                                   23 GGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELTCEDDPEWCIPGSIIVRYNLAN 82
                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS. SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN. SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted
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                                                                                                                                                      GGACGYKDVDKAPFLGMNSCGNDPIFKDGKGCGSCFEIKC-SKPEACSDKPALIHVTDMN 119
                              FHIEKASNPNYLALLVKYVAGDGDVVEVEIKEKGSEEWKALKESWGAIWRIDTPKPLKG-
                                                            IN----GNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQNWQSNT---YLRGQ 190
                                                                                         Theerakulpisut P., Goulding N., Suphioglu C., Singh M.B.,
                                                                                                                                                                                                                     55;
                                                                                                                                                                                                                                                                                263 AA;
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178
32
                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                   28497 MW;
                                                                                                                                                                                                                                    17.4%; Score 216.5; DB 1; 27.4%; Pred. No. 2.3e-12;
                                                                                                                                                                                                                        39; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                 EXPANSIN-LIKE CBD.
                                                                                                                                                                                                                                                                                                  N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                                                              MAJOR POLLEN ALLERGEN ORY S 1.
                                                                                                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                  B1C5F24EA398DD60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 AA
                                                                                                                                                                                                                                                       Length 263;
                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                       (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  and for
                                                                                                                                                                                                                             25;
                                                                                                                                                                                                                               Gaps
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ALD ALD ARRANGE ARE ARRANGED DE L'ARRANGE ARRANGE ARRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 8
                                                                                                                QY
δÃ
                                                         В
                                                                                                                                                                                Matches
                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase V)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P43317;
01-NOV-1995 (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Buropean Bioinformatics Institute. There are no restrictions on its the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Trichoderma reesei (Hypocrea jecorina).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saloheimo A., Henrissat B., Hoffren A.-M., Teleman O., Penttilae
"A novel, small endoglucanase gene, eg15, from Trichoderma reesei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=95075308; PubMed=7984103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=QM9414 / RUT C-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypocreales; Hypocreaceae; Hypocrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mol. Microbiol. 13:219-228(1994).
-!- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            isolated by expression in yeast.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pfam; pF00734; CBD_1; 1.
pfam; pF02015; Glyco_hydro_45; 1.
proDom; pD001821; CBD_fungal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z33381; CAA83846.1; HSSP; P00725; 2CBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (Cellulase V) (EG V).
                                                                                                                                                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR000254; CBD_fungal.
InterPro; IPR000334; Glyco_hydro_45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PROSITE; PS50842; EXPANSIN_EG45; 1.
PROSITE; PS01140; GLYCOSYL_HYDROL_F45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00236; fCBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cellulose degradation; Hydrolase; Glycosidase; Signal.
SIGNAL 1 17 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS00562; CBD_FUNGAL;
                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                            DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SIGNAL
   59 ELT----CEDDPEWCIPG-----SITVRYNLANFALANDNGGWCNPPL-----
                                                            25 YYDGQE-----GACGCGSSSGAFFWQLGIGNGVYTAAGSQALFDTAGASWCGAGCGKCY 78
                                                                                                                   12 FYGGADASGTMGGACGYGNLHSQ-----GYGLQTAALSTALFNS-----GQKCGACF 58
                                                                                                                                                                                                           POCGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TRIRE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HYDROLASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linkages in cellulose
                                                                                                                                                                                   38;
                                                                                                                                                                                                              Similarity
                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                   ĀΑ;
                                                                                                                                                                                                                                                                                                         24411 MW;
                                                                                                                                                                                                                 8.0%; Score 99; DB 1; 30.4%; Pred. No. 0.067;
                                                                                                                                                                                         11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                  BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                 CELLULOSE-BINDING (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRO/SER-RICH (LINKER).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOPHILE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENDOGLUCANASE V.
                                                                                                                                                                                                                                                                                                                                                                                              N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                                                                                                                      CC033FC51326C71D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       242 AA
                                                                                                                                                                                                                                                   DB 1; Length 242;
                                                                                                                                                                                                  28; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Penttilae M.;
                                                                                                                                                                                                        48; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
187 FIPMKSSWGAIWRIDPKKPLKG-PFSIRLTSEGGAHLVQDDVIPANWKPDTVYTSKLQFG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                    170 WQSMSRNWGQNWQSNTY--LRGQSLSFQVTDSDGRTVVSYDVVPHDW------QFG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                              127 KAGELTLQFRRVKCKYPSGTKITFHIEKGSNDHYLALLVKYAAGDGNIVAVDIKPRDSDE 186
                                                                                                                                                                  114 RAGIVPVAFRRVPCEKGGGIRFTIN----GNPYFDLVLITNVGGAGDIRAVSLKGSKTDQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ProDom; PD002179; Pollen_allergen; 1.
PROSITE; PS50843; EXPANSIN_CBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; S83343; AAB50734.2; -. HSSP; P43214; 1WHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -!- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS -!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN. -!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J. Allergy Clin. Immunol. 98:331-343(1996).
-- SUBCELLULAR LOCATION: Secreted.
-- DISEASE: CAUSES GRASS POLLEN ALLERGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cynodon dactylon (Bermuda grass).
Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC clade;
Chloridoldeae; Cynodonteae; Cynodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, 16-OCT-2001 (Rel. 40, 01-MAR-2002 (Rel. 41,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning and expression in yeast Pichia pastoris of a biologically active form of Cyn d 1, the major allergen of Bermuda grass pollen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Smith P.M., Suphioglu C., Griffith I.J., Theriault K., Knox R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MPC1_CYNDA
004701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CYNDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             interPro; IPR000882; Pollen_allergen.
                                                                                                                                                                                                                             77 KCK-EPVECSGEPVLVKITDKNYE-----HIAAYHFDLSGKAFGAMAKKGQEDKLR 126
                                                                                                                                                                                                                                                                                    61 TCEDDPEWCIPGSIIVRYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQ-----Y 113
                                                                                                                                                                                                                                                                                                                                                  18 WLEARATFYGSNPRGA-APDDHGGACGYKDVDKPPFDGMTACGNEPIFKDGLGCRACYEI 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Singh M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-96347957; PubMed-8757211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Major pollen allergen Cyn d 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      llergen.
                                                                                                                                                                                                                                                                                                                                                                                                      WERGHATTFYG----GADASGTWGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFEL 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PR01225; EXPANSNFAMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     246 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                145
240
9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26888 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 249.5;
Pred. No. 2.4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            43D8442DBA588322 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         246 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .4e-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      39;
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MP21_MAIZE
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                    Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                      110 LVKFVADDGDIVLMEIQDKLSAEWKPMKLSWGAIWRMDTAKALKG-PFSIRLTSESGKKV
                                                                                                                                                                                                                                                                                                                                                                                           ProDom; PD002179; Pollen_allergen; 1. PROSITE; PS50843; EXPANSIN_CBD; 1. PROSITE; PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR000882; Pollen_allergen. Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNFAMLY.
169 IAKDIIPANWR 179
                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L14271; AAA33496.1; -. PIR; JC1524; JC1524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPZ1_MAIZE
Q07154;
                               205 VSYDVVPHDWQ 215
                                                                                    147 LITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQNWQSNT--YLRGQSLSFQVTDSDGRTV 204
                                                                                                                                                                                                                                                                                                                                                                               Allergen; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MaizeDB; 65840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -!- DISEASE: CAUSES MAIZE POLLEN ALLERGY.
-!- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     rye grass.";
Gene 131:227-230(1993).
-!- TISSUE SPECIFICITY: POLLEN TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -1- DEVELOPMENTAL STAGE: EXPRESSION LOW BEFORE AND HIGH AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Broadwater A.H., Rubinstein A.L., Chay C.H., Klapper D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-94010312; PubMed-8406014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pollen allergen Zea m I (Zea m I)
                                                                                                                     50 YHFDLSGKAFGSLAKPGLNDKLRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGCNPNYVAV 109
                                                                                                                                                 99 -HFDLAEPAFLQIAQ-----YRAGIVPVAFRRVPCEKGGGIRFTIN----GNPYFDLV 146
                                                                                                                                                                                                                      40 TAALSTALENSGOKCGACFELTCEDDPEWCIPGSTIVRYNLANFALANDNGGWCNPPLK- 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Zea mI, the maize homolog of the allergen-encoding Lol pI gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Zea mays (Maize).
                                                                                                                                                                                      2 TACGNVPIFKDGKGCGSCYEVRCKEKPE-CSGNPVTVFITDMNY-----EPIAP 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POLLEN MITOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P43214;
                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                              191 AA;
                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                   105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Andropogoneae; Zea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                   186
                                                                                                                                                                                                                                                                                                                                 21362 MW;
                                                                                                                                                                                                                                                                         17.7%; Score 220; DB 1; 28.3%; Pred. No. 7.9e-13;
                                                                                                                                                                                                                                                             39; Mismatches
                                                                                                                                                                                                                                                                                                                                              EXPANSIN-LIKE EG45.
                                                                                                                                                                                                                                                                                                                            6E2A9DF921C45C63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         191 AA.
                                                                                                                                                                                                                                                                                              DB 1;
                                                                                                                                                                                                                                                                                           Length 191;
                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                         28;
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RACE REPORTED TO THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF THE PLANT OF T
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRINTS: PR01225; EXPANSNFAMIX.
ProDom; PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF01357; Pollen_allergen; l.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MPL1_LOLPR STANDARD; PRT; 263 AA.

P14946; P19964;
01-APR-1990 (Rel. 14, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pollen allergen Lol p 1 precursor (Lol p 1) (Allergen R7).
Lolium perenne (Perennial ryegrass).
Lolium perenne (Perennial ryegrass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=90375479; PubMed=1697854; Perez M., Ishioka G.Y., Walker L.E., Chesnut R.W.; Perez M., Cloning and immunological characterization o
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=4522;
                                                                                                                                                                                                                        Griffith I.J., Smith P.M., Pollock J., Theerakulpisut P., avjoglu A., Davies S., Hough T., Singh M.B., Simpson R.J., Ward L.D.,
                                                                                                                                                                                                                                                                              MEDLINE=91160716; PubMed=2001733;
                                                                                                                                                                                                                                                                                                                                                                                                                      allergen Lol p I.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               155 GAGELELQFRRVKCKYPDGTKPTFHVEKGSNPNYLALLVKYVDGDGDVVAVDIKEKGKDK 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    114 RAGIVPVAFRRVPCEKGGGIRFTIN----GNPYFDLVLITNVGGAGDIRAVSLKGSKTDQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                107
MEDLINE=86242068; PubMed=3718469;
                                                                                                             rye-grass pollen.";
FEBS Lett. 279:210-215(1991).
                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 24-48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       215
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      170 WQSMSRNWGQNWQSNT--YLRGQSLSFQVTDSDGRTVVSYDVVPHDWQ 215
                                                        SEQUENCE OF 24-53.
                                                                                                                                                                                                                                                                                                                 TISSUE-Pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63
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                                                                                                                                                                   "Cloning and sequencing of Lol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                u
                                                                                                                                                                                                                                                                                                                                                                                                  Biol. Chem.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDDPEWCIPGSIIVRYNLANFALANDNGGWCNPPLK--HFDLAEPAFLQIAQ-----Y 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WLDAKSTWYCKPTGAGPKDNGGACGYKDVDKAPFNGMTGCGNTPIFKDGRGCGSCFELKC 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WERGHATFYGGADASGTM--GGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELTC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WIELKESWGAIWRIDTPDKLTG-PFTVRYTTEGGTKAEFEDVIPEGWK 261
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    S80654; AAB35984.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      269 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                        265:16210-16215(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      30.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           35; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 257;
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                                                                                                                                                                               the major allergenic protein of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          263 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 269;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of the rye grass
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209 WIELKESWGAVWRIDTPDKLTG-PFTVRYTTEGGTKSEFEDVIPEGWK

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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cottam G.P., Moran D.M., Standring R.; "Physicochemical and immunochemical characterization of allergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SUBCELLULAR LOCATION: Secreted.
-!- DISBASE: CAUSES GRASS POLLEN ALLERGY.
-!- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Isolation and characterization of a major cross-reactive grass group
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Esch R.E., Klapper D.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=89364850; PubMed=2475768;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 236-263.
                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; M57474; AAA63279.1; -. EMBL; M57476; AAA63278.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR000882; Pollen_allergen. pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSHRAMLY.
                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS50843; PROSITE; PS50842;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ProDom; PD002179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          allergenic determinant.";
ol. Immunol. 26:557-561(1989).
 170 WQSMSRNWGQNWQSNT--YLRGQSLSFQVTDSDGRTVVSYDVVPHDWQ 215
                                                                                     101 -TKPESCSGEAVTV-----TITDDN----EEPIAPYHFDLSGHAFGSMAKKGEEQNVR 148
                                                                                                                                                                       5 WERGHATFYGGADASGIM--GGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELIC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      B37881; B37881.
S13614; S13614.
                                                          RAGIVPVAFRRVPCEKGGGIRFTIN----GNPYFDLVLITNVGGAGDIRAVSLKGSKTDQ 169
                                                                                                                                            WLDAKSTWYGKPTGAGPKDNGGACGYKNVDKAPFNGMTGCGNTPIFKDGRGCGSCFEIKC 100
                               SAGELELOFRRVKCKYPDDTKPTFHVEKASNPNYLAILVKYVDGDGDVVAVDIKEKGKDK
                                                                                                                EDDPEWCIPGSIIVRYNLANFALANDNGGWCNPPLK--HFDLAEPAFLQIAQ-----Y 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            P43214;
                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                            Glycoprotein;
                                                                                                                                                                                                                                                            263 AA;
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246
28
31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           EXPANSIN_EG45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EXPANSIN_CBD;
                                                                                                                                                                                                                                                             28438 MW;
                                                                                                                                                                                                                    20.4%; Score 254; DB 1
29.8%; Pred. No. 1e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Signal; Multigene family.
                                                                                                                                                                                                        37;
                                                                                                                                                                                                                                     P -> C (1... W -> WW (IN REF. 3).
W -> WW (IN REF. 3).
7675896F279C88C9 CRC64;
                                                                                                                                                                                                                                                                                                                                              N -> D.
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                                                                                                                                                                                                                                                                                                                                                                                        EXPANSIN-LIKE EG45
EXPANSIN-LIKE CBD.
                                                                                                                                                                                                                                                                                                                                                                                                                    POLLEN ALLERGEN LOL P 1.
                                                                                                                                                                                                                                                                                                                      v
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-> C (IN REF. 3)
-> WW (IN REF. 3
                                                                                                                                                                                                         Mismatches
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MPH1_HC
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01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Major pollen allergen Hol l 1 precursor (Hol
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schramm G.D., Bufe A., Petersen A., Haas H., Schlaak M., Becker "Mapping of IgE-binding epicopes on the recombinant major group allergen of velvet grass police, rHol 1 1."; J. Allergy Clin. Immunol. 99:781-787(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV. AVENEAE; TISSUE-Pollen; MEDLINE-97358126; PubMed-9215246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-96319506; PubMed-8768803; Schramm G.D., Petersen A., Bufe A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schramm G.D., Bufe A., Becker W.M., Schlaak M.; Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID-29679;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Holcus lanatus (Velvet grass).
                                                                                                    EMBL; Z27084; CAA81610.1; -. EMBL; Z68893; CAA93121.1; -. HSSP; P43214; IWHO.
                                                                                                                                                                                                                                                                                                                                                                                      This
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                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  entities requires a license agreement
                                                                                                                                                                                                                                                                                                                            the European Bloinformatics Institute.
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                         PRINTS;
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                                                                                   InterPro;
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                                                                                                                                                                                                                                                                                             SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way in the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the state of the st
Pro: TPR000882; Pollen_allergen.
Pr01357; Pollen_allergen; 1.
'S; PR01225; EXPANSEMANY.
'm; PD002179; Pollen_allergen; 1.
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D., Bufe A., Becker W.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-Pollen;
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                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
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01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Major pollen allergen Pha a 1 precursor (Pha a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MPA1_PH
Q41260;
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                                                                                                                                                                                                                                                                                                         pollen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phalaris aquatica (Canary grass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                       Suphioglu C., Singh M.B., Simpson R.J., Ward L., Knox R.B.; "Identification of canary grass (Phalaris aquatica) pollen by immunoblotting: IgE and IgG antibody-binding studies."; Allergy 48:273-281(1993).

-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                      Suphioglu C., Singh M.B.;
                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=96105569; PubMed=8564724;
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=28479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeac;
                                                                                                             -!- SÚBCELLULAR LOCATION: Secreted.
-!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
-!- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLI-
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                   MEDLINE=93319091; PubMed=7687099;
                                                                                                                                                                                                                                                                  SEQUENCE OF 30-49.
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                                                                                                                                                                                                                                                                                                                                      "Cloning,
                                                                                                                                                                                                                                                                                                                                                                                      rissue-Pollen;
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s requires a license agreement (See http://www.isb-sib.ch/announce/an email to license@isb-sib.ch).

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VS09_ROTHO
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Best Local Similarity Matches 70; Conserv

Conservative

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"Expansins are conserved in conifers and expressed in response exogenous auxin."
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U64891; AABA0635.1;
InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen:
1.
PRINTS; PR01225; EXPANSNFAMLY.
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Spermatophyta; Coniferopsida;
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01-MAY-1997 (TrEMBLrel. 03,
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ EMBL; U64893; AAB40637.1;
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Pfam; PF01357; PF011en_allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
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72.9%;
                                                             74.5%; Score 927; DB 10; 72.9%; Pred. No. 1.1e-78;
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Best Local :
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01-MAY-2000 (
01-MAY-2000 (
01-JUN-2001 (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hutchison K.W., Singer P.B., McInnis S., Diaz-Sala C., Greenwood "Expansins are conserved in conifers and expressed in hypocotyls response to exogenous auxin."; plant physiol 120:827-832(1999). EMBL: AF085330, AAD47901.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000882; Pollen_allergen. Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSURFAMIY. ProDom; PD002179; Pollen_allergen; 1. SEQUENCE 253 AA; 27150 MW; 2675BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-HYPOCOTYL;
MEDLINE-99329318; PubMed-10398718;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spermatophyta; Coniferopsida; NCBI_TaxID=3352;
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Eukaryota; Viridiplantae; St
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NWQSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSNWQFGQTFEGSQ
                                                     NWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQ
                                                                                                             ILYTRYPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVHAVSIKGSRSG-WOPMSRNWGO
                                                                                                                                       VAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQ 179
                                                                                                                                                                                                                       NDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIVP
                                                                                                                                                                                                                                                    EDDPEWCIPGSIIV---RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVP 119
                                                                                                                                                                                                                                                                                                                                    GGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMRC 88
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es; Pinaceae;
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Best Local (
                                                                                "Homolog to expansin in peach fruit.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AB029083; BAB19676.1;
InterPro; IPR000882; Pollen_allergen.
PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PP002179; Pollen_allergen; 1.
SEQUENCE 252 AA; 26743 MW; BF0B86FE0C060482 CRC64;
                                                                                                                                                                                                                                                                                                       Q9FS30;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (DEC-1997) to the EMBL/GenBank/DDBJ EMBL; AF038815; AAC33530.1; InterPro; IPR000882; Pollen_allergen. Pfam; PF01357; Pollen_allergen; 1.
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ProDom; PD002179; Pollen_allergen;
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SEQUENCE FROM N.A.
TISSUE-MESOCARP,
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                NCBI_TaxID=3760;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular cloning and nucleotide sequence from apricot fruit.";
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                                        Score 950.5; DB 1
Pred. No. 8.1e-81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                P93493
P93493;
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EMBL; AF159563; AAF21101.1; -.
InterPro; IPR000882; Pollen_allergen.
InterPro; IPR000408; RCC1.
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01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ProDom; PD002179; Pollen_allergen; 1. PROSITE; PS00626; RCC1_2; UNKNOWN_1.
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Pred. No. 3.3e-80;
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                                     Query Match
      Best Local Similarity
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                                                                                    PRINTS: PRO1225; EXPANSNEAMLY.
PRODOM: PD002179; Pollen_allergen; 1.
SEQUENCE 253 AA; 27260 MW; 08C428
                                                                                                                                                         Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC002336; AAB87577.1; ... InterPro; IPR000882; Pollen_allergen. Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-CV. COLUMBIA:
MEDLING-20083487; PubMed-10617197;
LLD X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Eugli C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
Slazberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of Chromosome 2 of the plant Arabidopsis
thallana.";
                                                                                                                                                                                                                                                                                                                                STRAIN-CV. COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JAN-1998 (TrEMBLrel. 05, 01-JAN-1998 (TrEMBLrel. 05, 01-DEC-2001 (TrEMBLrel. 19,
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Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
EMBL; U30382; AAB37746.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   118 VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNW 177
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      77.08;
74.38;
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                               Score 958.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
Pred. No. 1.5e-81;
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                                                                              08C42880D523DD8A CRC64;
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Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ291817; CAC19184 l;
InterPro; IPR000882; Pollen_allergen.
InterPro; IPR000881; RRM.
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                                                                                                                   211 NWGONWQSNSYLNGQPLSFQYTTSDGRTMTSYNVAPSNWQFGQTFQGAQF 260
                                                                                                                                                176 NWGONWOSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGOF 225
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ProDom; PD002179; Pollen_allergen; 1.
PROSTTE; PS00030; RRM_RNP_1; UNKNOWN_1
SEQUENCE 260 AA; 28266 MW; 32A7036
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Fabales; Fabaceae; Papillonoideae; Cicereae; Cicer.
                                                                                                                                                                              152 GIVPVSFRRVPCMKKGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSIKGSRTG-WQSMSR
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                                                                                                                                                                                                                                             94 RCNDDPRWCKPGSIIV--TATNFCPPNPSLANNNGGWCNPPLQHFDMAEPAFLQIAEYRA 151
                                                                                                                                                                                                                                                                          61 TCEDDPEWCIPGSIIVRYNLANF-----ALANDNGGWCNPPLKHFDLAEPAFLQIAQYRA 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 TCEDDPEWCIPGSIIVRYNLANF----ALANDNGGWCNPPLKHFDLAEPAFLQIAQYRA 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26 DDGGWQGGHATFYGGEDASGTMGGACGYGNLYGQGYGTNTAALSTALFNNGLTCGACYEM
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(TrEMBLrel.
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                                               PRELIMINARY;
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ProDom; PD002179; Pollen_allergen; 1
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Pfam; PF01357; Pollen_allergen; 1.
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Prunus armeniaca (Apricot).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases EMBL; U93167; AAC33529.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             muegute-A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.;
"Molecular cloning and nucleotide sequence of expansin 1 (PA-Exp1) from appricot fruit.";
Gribmitted inc.
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SEQUENCE FROM N.A.
TISSUE-MESOCARP PLUS EXOCARP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            spermatophyta; Magnoliophyta; eudicotyledons;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01225; EXPANSNFAMLY.
PRODOM; PD002179; Pollen_allergen;
SEQUENCE 254 AA; 27264 MW; 8806
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                             118 VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWOSMSRNW 177
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RCNNDPRWCRPGSIIVTATNFCPPNFAQSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGI 147
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                                                                                                                                                                                                                                                                              DNGGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFEL 60
                                                                                                                                                              TCEDDPEWCIPGSIIV----RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGI 117
                                                                                                                                                                                                                         DYGGWEGAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGSCYEM 87
                                                                                                               RCNNDPRWCRPGSIIVTATNFCPPNFAQSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGI 147
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                                                                                                                                                                                                                                                                                                                                                                      77.9%; Score 970; DB 10; 77.2%; Pred. No. 1.2e-82;
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                                                                                                                                                                                                                                                                                                                                              17; Mismatches
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Last annotation update)
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"Coordinated expression of genes encoding expansins and other cell
wall-modifying enzymes is associated with pectin-related changes in
the cell wall during ripening of cherry (P. cerasus) fruit.";
the cell wall during ripening of cherry (P. cerasus) fruit.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AR350936; AAK48845.1;
SEQUENCE 253 AA; 26861 MW; 9C24484F14AA52CD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EXP1
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Spermatophyta; Magnoliophyta; eudicotyledons;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q39625
                                                                                                                                                                                                                                                                  Cucumis sativus (Cucumber).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
      MEDITAE-96016146; PubMed=7568110; Shcherban T.Y., Shi J., Durachko D.M., Guiltinan M.J., Shcherban T.Y., Shi A., Cosgrove D.J.; McQueen-Mason S.J., Shieh M., Cosgrove D.J.; McQueen-Conserved, multigene family of proteins that mediate cell wall conserved, multigene family of proteins that mediate
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01-DEC-2001
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                                                                                                                                                         STRAIN-BURPEE PICKLER;
                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GONWOSNTYLRGOSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGOF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          VSFRRVSCVKKGGIRFTVNGHSYFNLVLITNVGGAGDVHSVSIKGSKTG-WQAMSRNWGQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DSDPKWCLPGSIIVTATNFCPPNLAQSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGIVP 148
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EDDPEWCIPGSIIV----RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVP 119
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(TrEMBLrel. 19, Last seq
(TrEMBLrel. 19, Last ann
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                                                                                                                                                                                                                                                                                                                                                                                                                                              (TrEMBLrel. 01, (TrEMBLrel. 19,
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edons; core eudicots; Rosidae;
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Q9LLB2;
01-OCT-2000
                                  Q9LLB2
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Arabidopsis thallana (Mouse-ear cress).
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Magnoliophyta; eudicotyledons; core eudicots; Rosid-
Spermatophyta; Magnoliophyta; eudicotyledons; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF0135/; FULL...
PRINTS; PR01225; EXPNISHFAMLY.
ProDom; PD002179; Pollen_Bllergen; 1.
ProDom; PD002179; POLLEN_BLLERGEN; 13E678633B2C4152 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Structural analysis of Arabidopsis thaliana chromosome 5. V. Sequence features of the regions of 1,381,565 bp covered by twenty one physically assigned Pl and TAC clones."; DNA Res. 5:131-145(1998).
EMBL: AB010692; BAB09972.1; -...
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Pfam; PF01357; Pollen_allergen; 1.
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                                                                                                                       178 GONWOSNTYLRGOSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
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                                                                                                                                                                                       VPVAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWOSMSRNW 177
                                                                                                                                                                                                                               QCEDDPEWCIPGSIIVSATNFCPPNFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGI 147
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(TrEMBLrel. 15, Created)
                               PRELIMINARY;
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96.1%;
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Im K.H., Cosgrove D.J., Jones A.M.;
"Subcellular localization of expansin mR
Plant Physiol. 123:463-470(2000).
EMBL; AF230332; AAF35901.1; -
InterPro: IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
SPECIES-P. Cerasus; TISSUE-RIPENING FRUIT; YOO S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.; "Coordinated expression of genes encoding expansins and other cell wall-modifying enzymes is associated with pecthr-related changes in the cell wall during ripening of cherry (P. cerasus) fruit."; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                           "Differential Expression of Expansin Genes Isolated from Sweet Cherry (Prunus avium L.) During Fruit Ripening.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
                                                                                                                                                                                                                                                                                                                                                                         Q9FUM3;
01-MAR-2001 (TrEMBLrel.
01-MAR-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                    Wu Z., Wiersma P.A.;
                                                                                                                                                                                                                                                                                                                          Prunus avium (Cherry), and
                                                                                                                                                                                                   SPECIES-P.avium;
                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                            Prunus cerasus
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                                                                                                                                                                                                                                                 NCBI_TaxID=42229, 140311;
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ProDom; PD002179; Pollen_allergen;
SEQUENCE 245 AA; 26201 MW; F661
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Pred. No. 9e-84;
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Listing first 45 summaries
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Maximum DB seq length: 200000000
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1: sp_archea:*
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1245
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  Gapop 10.0 , Gapext 0.5
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sp_plant:*
sp_vident:*
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sp_bacteria:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

16	15	14	13	12	11	10	9	œ	7	6	5	4	ω	2	 -	Result
923	927	927	927	944	950.5	954.5	957	958.5	962	963	970	972	982	1197.5	1203.5	Score
					76.3											Query Match I
232	253	232	232	253	252	252	260	253	250	253	254	254	245	255	255	Length I
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	DB
P93492	Q9SWY1	P93495	P93493	Q9SBT1	Q9FS30	081133	Q9FNT0	022874	Q39625	Q93XP2	082093	Q9FUM3	Q9LLB2	Q9FLC5	Q38866	ID
P93492 pinus caeda		bruns	spinus	Qysbti iragaria an	_	prunus				Q93xp2 prunus cera	prunus	prunus	Office zinnia ereg	_	Q38866 arabidopsis	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	
834	840	844	846	846	849	850	851	851	858	866.5	868	869	869	871	875	876	883	883	883.5	884	886	898	901	905	912	912	912	919.5	
														70.0													73.3		
257	260	258	260	250	239	262	257	249	255	249	248	250	237	253	252	249	251	246	242	246	247	251	249	247	258	249	232	253	
10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10	10							10	10	
Q9XGI6	Q93XP0	Q41043	Q9M2S9	Q9FVG9	Q9ZP31	080932	048818	Q9ZP36	Q9FMA0	Q9M515	080622	Q9C554	Q38863	Q94KT7	Q9FUM2	Q93XP1	Q40636	Q946J0	09LLB1	P93442	Q9M517	Q946J1	Q9ZP35	082625	049194	Q9LDR9	P93494	Q9SWD4	
60		0.04) (C	200	200	0.00	0.4	200	200	200	Ca	200	0.0				0.0			- T	L C	, Co	0.00		0 0		70	090	
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ALIGNMENTS

X m O	DR SQ	DR S	DR DR	RA RL	RA 7	Z Z	RL	RT:	₩ X -	RA	RA	RX F	D R	, ox	8	გ გ	80	GN	DE	D F	7 F	AC	ID	Q388	RESU
Ouery Match 96.7%; Best Local Similarity 96.5%; Matches 220; Conservative	ProDom; PD002179; Po SEQUENCE 255 AA;			McQueen-Mason S.J., Submitted (MAR-2001	Shcherban T.Y., Shi	[2]						MEDLINE=	ON [1]						EXPANSIN AT-	01-DEC-2001 (TrEMBLrel. 19,	01-NOV-1996 (TremBirel: 01,	Q38866;	D Q38866 PRELIMINARY;	Q38866	RESULT 1
96.7%; Score 1203.5; DB 10; Length 255; 96.5%; Pred. No. 2e-104; ive 1; Mismatches 4; Indels 3; Gaps	llen_allergen; 1. 27722 MW; 27B5F0827A285500 CRC64;	allergen; 1.	3.1; Pollen_allergen.	Shien M., Cosgrove D.J.;) to the EMBL/GenBank/DDBJ databases.			. U.S.A. 92:9245-9249(1995).		conserved, multigene family of proteins that mediate cell wall	<pre>McQueen-Mason S.J., Shieh M., Cosgrove D.J.; McQueen-Mason S.J., Shieh M., Cosgrove D.J.;</pre>	Shcherban T.Y., Shi J., Durachko D.M., Guiltinan M.J.,	Med=7568110;			II; Brassicales; Brassicaceae; Arabidopsis.	Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;	Arabidopsis thallana (Mouse-ear Cress). Arabidopsis thallana (Mouse-ear Cress).			19, Last annotation	01,		RY; PRT; 255 AA.	1	
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RESULT 15
AAR94532
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Best Local :
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26-OCT-1999;
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28-OCT-1999;
28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
        Expansins are a novel class of proteins that catalyse the extension of plant cell walls and the weakening of the hydrogen bonds in pure cellulose. 2 Expansins (AAR94528 and AAR94529) have been identified rice and 3 in Arabidopsis (AAR9430-32). A cDNA clone (AAR13320) coding for cucumber expansin 29 (AAR94527) has been obtd. Expansins can be used e.g. in the mfr., de-inking and recycling of paper, in the textile industry, to aid delignification processes, to alter gel
                                                                                                                      Expansin proteins which alter the mechanical strength of poly:saccharide(s) - useful in paper mfr. and recycling
                                                                                                                                                         WPI; 1996-201150/21
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12-MAY-1993;
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                                                                                                                                                                                                                                                                                                                                                             Expansin; plant cell wall; cellulose; paper recycling; de-inking;
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 mechanical strength,
                                                                                                 Disclosure; Page 32-33; 60pp; English.
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63.4%;
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Pred. No. 3.5e-68;
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Matches 137; Conserv
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Best Local
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182
                     186
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                                         VSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQN
                                                   VNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGAN
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WQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGW
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24; Mismatches 49
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hybridisation assay; genetic mapping; gene expression control; promoter;
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pathway; promoter;

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Best Local Similarity
Matches 135; Conserv
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39-CUT-1999
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                                      NYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGANW 186
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990S-0161361.
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                                                                                                                                                                                                                                                                                                            DB 21;
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09-MAR-1999

23-MAR-1999

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26-APR-1999

01-APR-1999

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21-APR-1999

21-AP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 65550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG51632;
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expression control;
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05-MAR 1999
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25-MAR 1999
25-MAR 1999
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17-MAY 1999
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19-MAY 1999
11-MAY 1999
11-JUN-1999
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Best Local Similarity 63.4
Matches 135; Conservative
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 197
                  187
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990S-015929.
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27; Mismatches 48;
 229
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99US-0154018.
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Pred. No. 2.9e
27; Mismatches
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ies 48;
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99US-0123180.
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99US-0139459. 99US-0139460. 99US-0139461. 99US-0139463. 99US-013963. 99US-0139750. 99US-0139750. 99US-0139817. 99US-0139817. 99US-0139817. 99US-0139819.	99US-0137724. 99US-0138094. 99US-0138647. 99US-0138847. 99US-0139452. 99US-0139453. 99US-0139454. 99US-0139456. 99US-0139456. 99US-0139457.	99US-0134221 99US-0134370 99US-0134768 99US-0134941 99US-0135124 99US-0135533 99US-0135629 99US-0136621 99US-013692 99US-0136782 99US-0137528 99US-0137528	99US-0127462 99US-0128714 99US-01288714 99US-0130077 99US-0130049 99US-013049 99US-0131449 99US-0132486 99US-0132486 99US-0132486 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487 99US-0132487	8 5 9 ≠
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Best Local Similarity 63.4%;
Matches 135; Conservative
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; Pred. No. 2.9e-68;
27; Mismatches 48
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        fragment SEQ ID
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         NO: 65551
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel nucleic acid sequences isolated from germinating seeds encoding polypeptides that are useful to control seed germination in plants \,
Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-PSDB; AAD03712.
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                           hybridisation assay; genetic mapping; termination sequence.
                                                       Protein identification; signal transduction pathway; metabolic pathway;
                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 3357.
                                                                                                                                                                      AAG06546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3; Page 49; 63pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                      standard;
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                                                                                                               (first entry)
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                                                                                                                                                                      Protein;
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Pred. No. 2.4e-70;
1; Mismatches 52;
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                                          gene expression control; promoter;
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 Lycopersicon esculentum
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                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                                                                             Arabidopsis thaliana
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                  25-FEB-2000; 2000EP-0301439.
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                                                                                                                                                                             Cucumber
                                                                                                                                        Expansin-29; plant cell wall; cellulose; paper recycling; de-inking;
polysaccharide; cucumber.
                                                                                                                                                                                                                                                     AAR94527 standard; Protein;
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        12-MAY-1995;
12-MAY-1993;
                                                                                                                   Cucumis sativus
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12-MAY-1993;
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                                            12-MAY-1994;
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        95US-0440517
93US-0060944
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93US-0060944.
                                            94AU-0068320
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                                                                                                                   var.
                                                                                                                   Burpee Pickler
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98.4%; Score 1178; DB 17; 100.0%; Pred. No. 8.3e-113;
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Best Local :
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 25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          other host cells. Expansin proteins have also been identified in out coleoptiles, in Arabidopsis (see AAR94530-32) and in rice (AAR94528-29), and appear to be broadly distributed throughout the plant kingdom. Expansins can be used e.g. in the mfr., de-lnking and recycling of paper, in the textile industry, to aid delignification processes, to alter gel mechanical strength, etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cucumber expansin-29 (AAR94527) is a member of a novel class of proteins that catalyse the extension of plant cell walls and the weakening of the hydrogen bonds in pure cellulose. It can be obto by expression of an isolated cDNA clone (see AAT13320) in bacterial or
                                                                                                                                                                                                                   Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter
                                                                                        25-FEB-2000;
                                                                                                                                                  EP1033405-A2
                                                                                                                                                                            Arabidopsis thaliana
                                                                                                                                                                                                                                                                  Arabidopsis thaliana protein fragment SEQ ID NO: 31249.
                                                                                                                                                                                                                                                                                                 17-OCT-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 7; Page 30; 60pp; English.
                                                                                                                                                                                                          termination sequence
                                                                                                                                                                                                                                                                                                                                                          AAG26696 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Expansin proteins which alter the mechanical strength of poly:saccharide(s) - useful in paper mfr. and recycling
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cosgrove DJ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VNYKRVPXORSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGAN
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99US-0121825.
99US-0123180.
99US-0123548.
99US-0125788.
99US-0126264.
                                                                                                                                                                                                                                                                                                                                                         Protein;
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64.58;
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Pred. No. 2.8
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Maximum Match 100%
Listing first 45 summaries
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Perfect score:
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seq length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-896-301-4
1197
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AAR94527
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                     Arabidopsis thalia
Tomato seed expans
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
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Cucumber expansin-
Arabidopsis thalia
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abidopsis thalia	Ar	AAG30326	21	210	5		45
is thal	Αı	AAG36446	21	210	6	77	44
idopsis that	Ar	AAG27399	21	191	6		43
idopsis thal	Ar	AAG27400	21	185	6.		42
idopsis tha		AAG36568	21	255	80	00.	41
is thal		AAG36569	21	249	ω.		40
is thal		AAG36570	21	242	œ	00.	39
idopsis thali		AAG46483	21	253	æ		38
idopsis thali		AAG25443	21	253	8		37
is thali		AAG05451	21	255	8	01.	36
s thali		AAG05452	21	249	8		S
s thali		AAG05453	21	241	8	01.	34
thal		AAG09620	21	280	8	02.	ω ω
s thali		AAG09621	21	258	8	02.	32
s thali		AAG09622	21	250	8	02.	31
ist		AAG26697	21	210	0	71	30
ed expan		AAE00412	22	263	0	19.	29
s thal		AAG30324	21	257	0.		28
s thal		AAG30325	21	255	0.	25.	27
is that		AAG29930	21	273	0.	27.	26
s thal		AAG29931	21	262	0	27.	25
s thal		AAG23850	21	282	<u>.</u>	31.	24
is thal		AAG43341	21	281		31.	23
s thal		AAG43342	21	253	μ.	31.	22
is tha		AAG23851	21	253		<u>3</u> 1.	21
bidopsis thal	Ar	AAG43343	21	251		31.	20
bidopsis thal	Ar	AAG23852	21	251	<del></del>	<u>3</u>	19
bidopsis thali	Ar	AAG36445	21	257		32.	18
e expansin.	R1	AAR94528	17	228	1.	ω ω	17
ato seed	To	AAE00414	22	250	ļ.	40.	16
is e	Ar	AAR94532	17	227		4	5
idops	Ar	AAG51645	21	280	.2	44.	14
is thali	Ara	5163	21	259	62.2	744.5	ω
is thali	Ara	AAG06544	21	259		44.	12

## ALIGNMENTS

Arabidopsis expansin

08-JUL-1996 AAR94530;

(first entry)

AAR94530 standard; Protein;

227

AA

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/note=
Misc-difference 214
                                                                          /note= "unidentified amino acid" Misc-difference 133
                                                                                      /note- "unidentified Misc-difference 104
                                                                                                       /note= "unidentified amino acid" Misc-difference 86
                                                                                                                                                            Expansin; plant cell wall; cellulose; paper recycling; de-inking; polysaccharide.
04-APR-1996
              AU9540262-A
                                    Misc-difference
                                                  Misc-difference
                                                                                                                                              Arabidopsis sp.
                                                                                                                           Location/Qualifiers
                             /note= "unidentified amino acids"
                                                          /note= "unidentified amino.acid"
                                           note= "unidentified"
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                                                                        "unidentified amino acid"
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EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTI Ver. 2.1
SEQ ID NO 3
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REQULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                    Matches 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Coggrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/092,160C CURRENT FILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: UNSURE
LOCATION: (14)..(58)
OTHER INFORMATION: Xaa is unknown or other.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
                                                               177
                                                                                                                                              117 MYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNW
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                                                                                   187 QSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
                                                                                                                                                                                      127 NYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGANW 186
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                                                                                                                                                                                                                               66 PQWCIK-GRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGIIPV 116
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                                                                                                                                                                                                                                                                                                                 NAHATTYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC-VND 65
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57.7%;
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Pred. No. 9.8e-56;
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RESULT 15
US-09-362-642-6
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                       APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
NUMBER OF SEQ ID NOS: 8
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Patent No.
SOFTWARE:
SEQ ID NO 6
                                                                                                                                                                                                                                                               Sequence 6, Application US/09362642 Patent No. 6350935
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ZIP: 94111-3834
COMPUTER READABLE FORM:
COMPUTEN READABLE FORM:
TYPE: Floppy disk
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LENGTH: 179 amino acids
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ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: PatentIn Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                    122 RVPCRKQGGIRFTINGFRYFNLVLITNVAGAGDIVRVSVKGSNTGWMSMSRNWGQNWQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                            130 RVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGANWQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10 ATTYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCDTSQTKW
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REFERENCE/DOCKET NUMBER: 023070-078200US
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o. 5929303
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                     PatentIn Ver. 2.1
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) 576-0300
NO: 6:
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Pred. No. 9.2e-54;
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APPLICANT: Guiltinan, Mark J APPLICANT: Shcherban, Tatyana

APPLICANT: Shi, Jun

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; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis ; OTHER INFORMATION: expansin US-09-092-160-5
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US-08-845-539-2
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Best Local Similarity
Matches 122; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EARLIER APPLICATION NUMBER: 08/440,517 EARLIER FILING DATE: 1995-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EARLIER FILING DATE: 1993-05-12 NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS FILE REFERENCE: 1194/1C114US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence FEATURE:
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APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture
NUMBER OF SEQUENCES: 8
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                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                  CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
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STATE: California
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                                                            FILING DATE:
                                                                          APPLICATION NUMBER:
                                                                                                                    SOFTWARE: PatentIn Release #1.0, Version #1.30
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                                                                                                                                                                                                                                                                                                              ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIPGS---IIVRYNLA--NFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVPVAFR 123
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Bastian, Kevin L.
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                                                          25-APR-1997
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57.8%;
                                                                              US/08/845,539
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Pred. No. 7.6e-57;
                                                                                                                                                                                                                                                                                                                                                                     Control Fruit Texture and Softening
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                                                                   TOPOLOGY: US-08-440-517A-3
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 Matches
                 Best
                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-078200US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 222
                                                                                                                                                                                                                     CURRENT APPLICATION DATA
                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214 NWQSNAVLTGQS 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     154 PVTYRRIPCRKQGGIRFTINGFRYFNLVLITNVAGAGDIIKVWVKGTKTNWIPLSRNWGQ 213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   125 PVNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGA 184
               Local Similarity
                                                                                                                                                                                                                                                                                                                                                   CITY: UNIVERSITY PARK STATE: PENNSYLVANIA
                                                                                                   TYPE:
                                                                                                                                                                 CLASSIFICATION: 530
                                                                                                                                                                                    FILING DATE:
                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                ZIP: 16802-7000
                                                                                                                                                                                                                                                                                                                                COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY STREET: 113 TECHNOLOGY CENTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX:
                                                                                                                                                                                                  APPLICATION NUMBER: US/08/440,517A
                                                                                                                                                                                                                                                  OPERATING SYSTEM:
                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   94 PNWKWCLPGNPSILITATNFCPPNYALPNDNGGWCNPPRPHFDLAMPMFLKLAQYRAGIV 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     34 ETAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGLSCGACFELKCTNT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SQTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIV 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114;
                                                                                                  AMINO ACID
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                                                                                                                                                                                                                                                                                                                                   UNITED STATES OF AMERICA
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 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SHCHERBAN, TATYANA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COSGROVE, DANIEL J.;
                                                                                                                                                                                                                                                                    NEC
                                                                                                                                                                                                                                     WORDPERFECT 5.1
                                                                                  UNKNOWN
                                                                                                                                                                                                                                                                                   FLOPPY DISK
                                                                                                                                                                                                                                                                  286
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54.2%; Score 649; DB 2; 57.7%; Pred. No. 9.8e-56; Mismatches 55;
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Pred. No. 1.2e-56;
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                               Length 222;
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EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTMARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 228
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SEQ ID NO 2
LENGTH: 225
TYPE: PRT
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Best Local
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                                                                                                                                                                           Matches
                                                                                                                                                                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
CURRENT PILING DATE: 1999-07-27
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: PRT ORGANISM: Artificial Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  124 AYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQNW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127 NYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGANW 186
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                                                                                           34 ETAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGLSCGACFELKCTNT 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 SAFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTTTCDTSQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Match 61.3%; ocal Similarity 63.8%;
              94 PNWKWCLPGNPSILITATNECPPNYALPNDNGGWCNPPRPHFDLAMPMELKLAQYRAGIV 153
                                                  65 SQTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIV 124
                                                                                                                6 OSAFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITC-DT 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115;
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                                                                                                                                                                             Conservative
                                                                                                                                                                                                55.4%; score 663.5; DB 4; Length 225; 59.9%; Pred. No. 3.9e-57;
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                                                                                                                                                                             32; Mismatches
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                                                                                                                                                                                 44; Indels
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                                     US-09-092-160-5
                                                       RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Sequence 5, Application US/09092160C Patent No. 6255466
                                                                                                                                                                                                                                                                                                                                                                                                   Matches 122;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: PU NUMBER OF SEQUENCES: 6 CORRESPONDENCE ADDRESS:
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MEDIUM TYPE: FLOPPY DISK
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                                                                                                                                                                                                                  130 RVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTG-WMAMSRNWGANWQS 188
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ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
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                                                                                                                                                                                                                                                                                                                             10 ATTYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALTNSGQKCGACTELTCE-DDPEW 68
                                                                                                                                                                                                                                                                                                                                            10 ATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTTTCDTSOFKW 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/440,517A
                                                                                                                                                                                                                                                        69 CIPGS---IIVRYNLA--NFALANDNGGWCNPPLKHEDLAEPAFLQIAQYRAGIVPVAFR 123
                                                                                                                                                                                                                                                                                        70 CKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVPVNYK 129
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE
                                                                                                                                 NAYLAGOSLSFIVQLDDGRKVTAWNXAPXNW 219
                                                                                                                                                                                RVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQNWQS 183
                                                                                                            NTYLRGOSLSFOVTDSDGRTVVSYDVVPHDW 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AMINO ACID
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  UNITED STATES OF AMERICA
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                                                                                                                                                                                                                                                                                                                                                                                                       33; Mismatches
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GENERAL INFORMATION:

APPLICANT: Cosgrove, Daniel J APPLICANT: McQueen-Mason, Simo

Simon

TOPOLOGY:

UNKNOWN

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us-09-092-160-6
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                                                                                                                                                                                                                                                                                                                                  Matches 137;
                                                                                                                                                                                                                                                                                                                                                                        Query Match
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CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
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EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
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APPLICANT: Guiltinan, Mark J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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                                                               122 VSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQN 181
                            186 WQSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
                                                                                                     126 VNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGAN 185
                                                                                                                                                64 DGQWCLPG--SVTVTATNICPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGIVP 121
                                                                                                                                                                         66 QTKWCKPGGNSITITATNICXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVP 125
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Local Similarity 64.0%;
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        Conservative
                                                                                                                                                                                                                                                                                                                     62.0%; Score 742; DB 4; Length 226; 64.0%; Pred. No. 8.9e-65; tive 24; Mismatches 49; Indels
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                                APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
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                                                                                              APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
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APPLICANT: McQueen-Mason, Simon
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CURRENT FILING DATE: 1998-06-05
          CURRENT APPLICATION NUMBER: US/09/092,160C
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ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
                                                                                                                                                                                                                                                                                                                              184 QSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGW 216
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63.8%; Pred. No. 6e-64;
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EARLIER APPLICATION NUMBER: 08/440,517
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PACENTIN Ver. 2.1
SEQ ID NO 4
LENGTH: 227
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US-09-092-160-7
; Sequence 7, Application US/09092160C
; Patent No. 6255466
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APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/IC114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
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                      GENERAL INFORMATION:
APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
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Best Local Similarity
Matches 220; Conserv
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      TITLE OF
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NAME/KEY: UNSURE
LOCATION: (2)..(227)
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: Shi, Jun invention: PURIFIED EXPANSIN PROTEINS
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CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
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GENERAL INFORMATION:
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SEQ ID NO 7
LENGTH: 227
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                                                                 CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: SHCHERBAN, TATYANA;
APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
TYPE OF THE
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                                                                                                                                                              COMPUTER: NEC 286
OPERATING SYSTEM: DOS
SOFTWARE: WORDDERFECT 5.1
CURRENT APPLICATION DATA:
                      SEQUENCE CHARACTERISTICS:
LENGTH: 226
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
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APPLICANT: GUILTINAN, MARK;
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                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: INTELLECTUAL PROPERTY OFFICE,
ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
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                                                                                                                 APPLICATION NUMBER: US/08/440,517A FILING DATE:
                                                                                                                                                                                                                                                                                                              ZIP: 16802-7000
                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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Score 1178; DB 2; L pred. NO. 3.2e-107; 0; Mismatches 0; SGACGYGNLYNAGYGLYNAALSS 	OVE, DANIEL J.; INAN, WARK; INAN, WARK; JUN PURIFIED EXPANSIN PROTEINS ES: 6 ES: 6 ENESS: 7 ELLECTUAL PROPERTY OFFICE, THE NSYLVANIA STATE UNIVERSITY CCHNOLOGY CENTER TY PARK VANIA D STATES OF AMERICA 10 STATES OF AMERICA 10 STATES OF AMERICA 11 DOS 15 ON DATA: ON DATA: ON DATA: S30 ID NO: 4: RISTICS:	ALIGNMENTS	US-08-441-507-24 US-08-441-507-5 US-08-441-507-4 US-08-441-507-23 PCT-US-6-09848-21 US-08-486-036A-4 PCT-US-6-09848-24 US-08-486-036A-2 PCT-US-6-09848-24 US-08-482-282B-4 US-08-482-282B-4 US-08-481-974-4 US-08-433-888-4 US-08-174-739A-4 US-08-411-777-10 US-09-057-088-10
### Page 18			Sequence 24, Appli Sequence 4, Appli Sequence 23, Appli Sequence 21, Appli Sequence 24, Appli Sequence 24, Appli Sequence 24, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 27, Appli Sequence 28, Appli Sequence 29, Appli Sequence 29, Appli Sequence 20, Appli Sequence 21, Appli Sequence 22, Appli Sequence 24, Appli Sequence 24, Appli Sequence 26, Appli Sequence 27, Appli Sequence 28, Appli Sequence 29, Appli Sequence 29, Appli Sequence 29, Appli Sequence 20, Appli Sequence 21, Appli Sequence 21, Appli Sequence 21, Appli
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                                                                                                                                                                                                                                                                                                                        R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library. July 1996
A;Description: Expansins are conserved in conifers and expressed A;Reference number: Z16866
A;Accession: T09825
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                      expansin (clone pPtexp4) - loblolly pine (fragment)
c;Species: Pinus taeda (loblolly pine)
c;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C;Accession: T09825
R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
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T09825
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A; Gene: expl8
C; Superfamily: expansin
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A; Residues: 1-232 <HUT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C:Species: Lycopersicon esculentum (tomato)
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 20-Jun-2000
C:Accession: T06573
R:Reinhardt, D.; Wittwer, F.; Mandel, T.; Kuhlemeier, C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: EMBL: AJ004997; PIDN: CAA06271.1
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A; Residues: 1-255 < REI>
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66 QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVP 125
                                               11
                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89 YPQWCHPGSPSIFITATNFCPPNFALPNDNGGWCNPPRPHFDLAMPMFLHIAEYRAGIVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6 QSAFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCDTS 65
                                          ESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMQCN-D 69
                                                                 WQSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WQTNSVLFGQSLSFRVRAGDRRSSTSWNTTPAHW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VVYRRVPCRKQGGIRFTINGFRYFNLVLVTNVAGAGDIVSLSIKGSKTNWISMSRNWGQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSAHATFYGGSDASGTMGGACGYGNLYSQGYGVNNGALSTALFNNGLSCGACFEIKCD-N
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                                                                                                                                                      61.6%; Score 737.5; 63.1%; Pred. No. 3e
                                                                                                                               24; Mismatches
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                                                                                                                                                      3e-56;
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                                                                                                                                                                          DB 2;
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                                                                                                                             52;
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                                                                                                                                                                      Length 232;
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                                                                                                                                                                                                                                                                                                                                                                    F;25-258/Product: expansin #status predicted <MAT>
                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: expansin F;1-24/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                           A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                               C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: cv. Burpee Pickler; hypocotyl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Cross-references: EMBL: U30460; NID: g1040876; PIDN: AAB37749.1; PID: g1040877
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: mRNA
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Best Local
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                                    186
                                                                     152 LYQRVPCKKRGGVRFTVNGRDYFELVLITNVGGAGDIKSVSIKGSKSSNWTPMSRNWGAN
212 WQSNSYLNGQSLSFKVTTSDGQVQVFNNVVPSSW 245
                                                                                              127 NYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGS-NTGWMAMSRNWGAN 185
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                                                                                                                                                93
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                                                                                                                                                                                                                     33 AHATFYGESDASGTMGGACGYGNLYQTGYGTRTAALSTALFNDGASCGQCFKIICDYKTD 92
                                                                                                                                                                                                                                                                                                              Local Similarity
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                                                                                                                                                                                                                                        8 AFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCD-TSQ 66
                                  WQSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
                                                                                                                                                                                 TKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVPV 126
                                                                                                                                              PRWCIKGA-SVTITATNFCPPNYALPNNNGGWCNPPLKHFDMAQPAWQKIGIYRGGIIPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | DPQWCLPG--TVTITATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIVP 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                VNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGAN 185
                                                                                                                                                                                                                                                                                                                                                                                                                           induces cell wall extension in plants
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                                                                                                                                                                                                                                                                                                            61.5%;
61.7%;
                                                                                                                                                                                                                                                                                            28; Mismatches
                                                                                                                                                                                                                                                                                                            Score 736.5; DB : Pred. No. 4.1e-56
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A:Introns: 52/1; 158/2
A:Note: T22E16.160
C:Superfamily: expansin
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N;Alternate names: protein T22E16.160
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
C:Accession: T47689
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A;Molecule type: DNA
A;Residues: 1-260 <BEN>
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A; Accession: T47689
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A:Molecule type: mmRNA
A;Residues: 1-257 <CADD
A:Cross-references: EMBL:AJZ43340; PIDN:CAB46492.1
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                                                                                                        186 WQSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
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                                                                                                                                                                   154 ISYRRVACRKSGGIRFTINGHRYFNLVLITNVAGAGDIARTSVKGSKTGWMSLTRNWGQN 213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.; Mayer,
                                                                                                                                                                                                                                                                                                                                                                                                                               QSAFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCDTS 65
                                                    WQSNAVLVGQSLSFRVTSSDRRTSTSWNIAPSNW 247
                                                                                                                                                                                                                                                                                                                                                                                                    QTAHATFYGGNDASGTMGGACGYGNLYSQGYGTNTAALSTSLFNSGQSCGACFEIKC-VN 93
                                                                                                                                                                                                                                                                                                                                         QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVP 125
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Pred. No. 5.7e-57;
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A; Residues: 1-264 < LEE>
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C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000
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A;Accession: T04175
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Status: preliminary; translated from GB/EMBL/DDBJ
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         157 PVSYRRVPCRKKGGVRFTINGFRYFNLVLITNVAGAGDIVRASVKGTSTGWMPMSRNWGQ 216
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                142 VSFRRVPCVKKGGIRFTVNGHSYFNLVLVTNVAGAGDVRSVSIKGSRTGWQPMSRNWGQN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     126 VNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGAN 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVP 125
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                                                                                                                                                                                                                                                                        6 QSAFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITC-DT 64
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                                                                                                                                                   PVNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGA 184
                                                                                                                     PGWEWCHPGSPSILITATNFCPPNYALPSDNGGWCNPPRPHFDLAMPMFLHIAEYRAGIV 156
                                                                                                                                                                                                                                          QSAHATFYGGSDASGTMGGACGYGNLYSQGYGVNNAALSTALENSGQSCGACFEIKCVNQ 96
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Pred. No. 1.3e-56;
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expansin (clone pPtexp3) - loblolly pine (fragment) C;Species: Pinus taeda (loblolly pine) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #C;Accession: T09821 C;Accession: T09821 Singer, P.B.; Diaz-Sala, C.; Gree submitted to the EMBL Data Library, July 1996 A;Reference number: Z16866 A;Reference number: Z16866 A;Accession: T09821
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C;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C;Accession: T09826
R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.: Greenwood M c
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                                             A;Description: Expansins are conserved in conifers and A;Reference number: Z16866
A;Accession: T09826
A;Status: preliminary; translated from GB/EMBL/DDBJ
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A;Experimental source: clone pPtexp3
                                                                                                                   R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M. submitted to the EMBL Data Library, July 1996
                                                                                                                                                                                                                                                                                                   밁
A;Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105
              A; Molecule type: mRNA
A; Residues: 1-232 < HUT>
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Best Local
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                                                                                                                                                                                                                                                                                                     WQSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSNW
                                                                                                                                                                                                                                                                                                                                    WQSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
                                                                                                                                                                                                                                                                                                                                                                         ILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVHAVSIKGSRSGWQPMSRNWGQN 187
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVP 125
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       A; Accession:
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expansin (clone pPtexp2) - loblolly pine (fragment) C;Species: Pinus taeda (loblolly pine) C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 C;Accession: T09818
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Experimental source: clone pPtexp5 C;Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library, July 1996
A;Description: Expansing are conserved in conifers and expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: (C; Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL: U64890; NID: g1778098; PID: g1778099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-232 <HUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T09818
                                                                                                  C;Species: Lycopersicon esculentum (tomato)
C;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Status: translated from GB/EMBL/DDBJ
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                                     R;Caderas, D.M.
submitted to the EMBL Data Library, June 1999
                 A; Reference number:
                                                                                C; Accession:
                                                                                                                                           expansin 9 [imported] - tomato
                                                                                                                                                                   T50658
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                                                                                                                                                                                                                                                                                                                                       ILYTRVPCLRKGGIRFTVNGHSYFNLVLTTNVGGAGDVHAVSIKGSMSGWQPMSRNWGQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVP 125
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                                                                                                                                                                                                                                                                                            WQSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
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63.1%;
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Pred. No. 2.3e-57;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pred. No. 4.2e-57;
Mismatch
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A;Accession: T10079
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-250 <SHC>
A;Cross-refe: 1-250 <SHC>
A;Experimental source: cultivar Burpee Pickler
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O. Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; D. ansen, N.F.; Hughes, B.; Huizar, L. Nature 408, 816-820, 2000

A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E. C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H. A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis. A;Accession: F86335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Gene: EXP1
C;Function:
A;Description: mediates cell wall extension
A;Superfamily: expansin
E;1-23/Domain: signal sequence #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 hypothetical protein T20H2.4 [imported] - Arabidopsis thaliana C;Speciles: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001 C;Date: 05-Mar-2001 #sequence_revision 05-Mar-2001 #text_change 31-Dec-2001 C;Accession: F86335
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C; Superfamily:
                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE005172; C;Genetics:
                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-252 <STO>
                                                                                                                                                                                                                                                                                                                                                                                   A; Status: preliminary
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                                                                                                                        4 VAQSAF-----ATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMC 54
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGAN 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DPKWCLPG--TIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQTAQYRAGIVP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNW 239
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                   GECYRITCDHAADSRWCLKGA-SVVITATNFCPPNFALPNNNGGWCNPPLKHFDMAQPAW 134
                                                         GACYTITCD-TSQTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAW 113
                                                                                                 IAVDAFRPSGLTNGHATFYGGSDASGTMGGACGYGDLYSAGYGTMTAALSTALFNDGASC 75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               138;
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                                                                                                                                                                                                   Score 764.5; DB 2
Pred. No. 1.6e-58;
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R;Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Shi proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A;Title: Molecular cloning and sequence analysis of expansins--a highly conserved, mu A;Reference number: Z14894; MUID:96016146
A;Accession: T03298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C; Species: Oryza sativa (rice)
C; Date: 24-Mar-1999 #sequence_
                                                                                                                                                                                                                                            C;Accession: T03737
R;Cho, H.T.; Kende, H.
Plant Cell 9, 1661-1671, 1997
A;Title: Expression of expansin genes is correlated with A;Reference number: 215042; MUID:97480100
A;Accession: T03737
                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
T03737
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-251 <SHC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Accession: T03298
                                                              A; Gene: RiExA C; Superfamily:
                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-261 <CHO>
                                                                                                                                                                                                                                                                                                                                                                                                                                    expansin - rice
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Description:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: EXP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expansin 2 -
                                                                                                                                                        A;Cross-references: EMBL:Y07782; NID:g2924246; PIDN:CAA69105.1; PID:g2924247
                                                                                                                                                                                                                           A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                        C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                              C; Species: Oryza sativa (rice)
                                                                                                                                    A; Experimental source: subsp. Japonica, cv, Nipponbare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                               Genetics:
Best Local Similarity
                   Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    66 QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVP 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 QSAFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTTTCDTS
                                                                                           RiExA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENIAVYQAGIVPVNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNT 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GWLAMSRNWGANWQSNAYLDGQALSFSITTTDGATRVFLNVVPSSW 240
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WQSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQN
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63.28;
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Pred. No. 2.3e-58;
Score
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                   Length 261;
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Result
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     on:
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Copyright (c) 1993 - 2002 Compugen
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(without alignments)
1914.721 Million cell updates
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                       expansin-like expansin EXP2
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n S1 precur
                                                                  - upland
expansin
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C; Function:
A; Description: i
C; Superfamily: 6

expansin

extension (creep) in plant

cell

walls

Shi

₫

Matches Query Match Best Local

214;

Conservative

0,

Score 1173; DI Pred. No. 1.1e. 0; Mismatches

.1e-93 DB

2; 5

Length 255; Indels

0;

Gaps

0,

Similarity

98.0%; 97.7%;

1 KXSVAQSAFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTI

KXSVAQSAFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYT1

83

TCDTSQTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQ

TCDTSQTKWCKPGGNSITITATNLCPPNWALPSNSGGWCNPPLQHFDMSQPAWENIAVYQ

143

A; Gene: EXP3

Shi

∄u

RESULT

Qy В QΥ Вb QУ Вb 20

121 AGIVPVNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSR

AGIVPVNYKRVPCQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSR

84 61 24

204 181 144

NWGANWQSNAYLAGQSLSFIVQLDDGRKYTAWNXAPXNW 219

RESULT 1 T03299 expansin 3 - rice C;Species: Oryza sativa (rice) C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000 C;Accession: T03399 R;Shcherban, T.V.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; R;Shcherban, T.V.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; A;Ritle: McLecular cloning and sequence analysis of expansinsa highly conserved, A;Reference number: 214894; MUID:96016146 A;Accession: T03299 A;Status: preliminary: translated from GB/EMBL/DDBJ A;Molecule type: mRNA A;Residues: 1-255 <shc> A;Cross-references: EMBL:U30479; NID:g1041711; PIDN:AAB38075.1; PID:g1041712 C;Genetics:</shc>	ALIGNMENTS	30 692.5 57.9 255 2 T02010 expansin homolog T   31 670 56.0 255 2 T80655 expansin in homolog T   32 626.5 52.3 257 2 F86259 protein T12C24.10   33 600.5 50.2 257 2 G96654 hypothetical protein   35 503.5 42.1 256 2 T05648 expansin homolog T   36 233 19.5 491 2 F96681 expansin homolog T   37 229.5 19.2 259 2 T50657   38 229.5 19.2 259 2 T50657   39 229.5 19.2 259 2 T84859    39 221 18.5 259 2 E84886
en-Mason, S.J.; Sighly conserved,		nsin homolog T in EXP5 [imp ein T12C24.10 thetical prote nsin - upland nsin homolog F ein F1E22.6 [i -expansin [imp expansin [imp bable beta - expa abin (clone pp nosin (clone pp protein - soy protein homol nsin (clone pp protein homol nsin (clone pp protein homol nsin (clone pp protein homol nsin (clone pp

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Search completed: October 11, 2002, 14:57:32 Job time: 7.86347 secs
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ID ENV2_MOUSE
AC P11370;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-85265041; PubMed=2991595;

Ikeda H., Laigret F., Martin M.A., Repaske R.;

"Characterization of a molecularly cloned retroviral sequence associated with FV-4 resistance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
01-NOV-1991 (Rel. 20, Last annotation update)
Retrovirus-related ENV polyprotein (FV-4 locus) (Fragments).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PRO0429; ENV_polyprotein; 1. Coat protein; Polyprotein. NON_CONS 348 349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; M11051; AAA37562.1; -. EMBL; M11052; AAA37563.1; -. PIR; A25483; A25483.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Virol. 55:768-777(1985).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                       164 CGGPEAYYCASWGCETTGRAAWKPTSSWDYITVSNNLSSPQAPKACKNNGWCNPLVVRF- 222
                                                                                                                                                         223 -TGPG-------KRATSWTTGHEWGLRLYISGHD 248
                                                                                                                                                                                                                                    108 MSQPAWENIAVYQAGIVPVNYKRVPXQRSG---GIRFAISGHD 147
                                                                                                                                                                                                                                                                                                                                                                                             54 CGA-----CYTITCDTSQTKWCKPGGNSITIT-ATNLCXPNWALPSNSGGWCNPPLXHFD 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          348 349
432 AA; 47661 MW; 092D3963EE5771FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.1%; Score 84.5; DB 1; Length 432; ilarity 28.2%; Pred. No. 2.3; Conservative 10; Mismatches 37; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27; Gaps
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ENV_FLVLB STANDARD, AC P11261; Q85515; Q85516; DT 01-JUL-1989 (Rel. 11, C)
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SEQUENCE
                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
MEDLINE-88036192; PubMed-2444714;
NICOlalsen-Strouss K., Kumar H.P.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUL-1989 (Rel. 11, Created)
01-JUL-1989 (Rel. 11, Last sequence update)
16-CCT-2001 (Rel. 40, Last annotation update)
ENV_polyprotein precursor (Coat polyprotein)
                                                                                                                                                                                                          EMBL; J03448; AAA43048.1; -. PIR; A27172; VCMVLB.
                                                                                                                                                                                                                                                                                                                                                binding epitope.";
J. Virol. 61:3410-3415(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GP70; Spike protein P15E] (Fragment).
                                  CARBOHYD
                                                         CARBOHYD
                                                                     CARBOHYD
                                                                              CARBOHYD
                                                                                           CARBOHYD
                                                                                                    CARBOHYD
                                                                                                                                                  SIGNAL
                                                                                                                                                            Coat protein;
                                                                                                                                                                          InterPro; IPR002050;
Pfam; PF00429; ENV_pc
                                                                                                                                                                                                 HSSP; P03385; 1MOF
                                                                                                                                                                                                                                                                                                                                                                                                Elder J.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; Retroid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Feline leukemia virus (strain B/lambda-B1).
                                                                                                                                                                                                                                                                                                                                      -!- PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
                                                                                                                                                                                                                                                                                                                                                                       nonocional antibody via an
                                                                                                                                                                                                                                                                                                                                                                                   'Natural feline leukemia virus variant escapes neutralization by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GPQDGFCAVWGCETTGETYWRPTSSWDYITVKKGVTQGIYQC-----SGGGWCGPCYD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGKDGSCTMGGACGYGNLY------NAGYGLYNAALSSALFNDGAMCGACYT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ITCDTSQTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMS--QPAWENIA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
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                                  466
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                                                                                                                                                            Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -----PKSWGLRLYRSGYDPIALFSVS 234
                                                                                                                                                                      02050; Env_polyprotein.
ENV_polyprotein; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   viruses; Retroviridae; Gammaretrovirus
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534
58348
                                  465
662
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286
286
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327
351
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          73132
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            ME.
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X
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                                                                                                                                                            Polyprotein; Signal
                                           N-LINKED
                                                                            N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pred.
                                                                                                                           KNOB PROTEIN GP70.
SPIKE PROTEIN P15E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 85.5;
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                                                                    N-LINKED
                                                                                                    N-LINKED
                                                                                                                  N-LINKED
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            D4AC18E197230575
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O
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                                (GLCNAC
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            CRC64;
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                                                                 (POTENTIAL).
(POTENTIAL).
(POTENTIAL).
                                (POTENTIAL)
                                                                                                              (POTENTIAL).
                                                       (POTENTIAL)
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16-OCT-2001 (Rel. 4
01-MAR-2002 (Rel. 4
Endoglucanase (EC 3
                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                         Cellulose
ACT_SITE
ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu B., Hellman U., Ersson B., Janson J.-C.;

*Purification, characterization and amino-acid sequence analysis of thermostable, low molecular mass endo-beta-1,4-glucanase from blue mussel, Mytilus edulis.*

Eur. J. Biochem. 267:4970-4977(1999).

Eur. J. Biochem. 267:4970-4977(1999).

-I- FUNCTION: ACTIVE TOWARDS THE SOLUBLE CARBOXYMETHYLCELLULOSE (CMC).

POSSESSES EXPANSIN ACTIVITY TOO.

-I- CAPALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-OCT-2001
16-OCT-2001
                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                        DISULFID
                                                                                                                                                                                                                                                                                                                                                                              -i- TISSUE SPECIFICITY: DIGESTIVE GLAND.
-i- MASS SPECTROMETRY: MW-19702; METHOD-MALDI.
-i- MISCELLANEOUS: Has an isoelectric point of 7.6. Its optimum pH is
4.6 and optimum temperature is between 30-50 degress celsius.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE-Digestive gland; MEDLINE-20389517; PubMed-10931178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mytilus edulis (Blue mussel).
Eukaryota; Metazoa; Mollusca; Bivalvia; Pteriomorphia; Mytiloida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GUN_MYTED
                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                               DISULFID
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                                                                                                                                                                                                                                                                                                                                     InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=6550;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mytiloidea; Mytilidae; Mytilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CMCASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                118 VYQAGIVPVNYKRVPXQRSGGIRFAISGHDYFELVTVT 155
69
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                                                                                                                                                                                                                                                                                                                                                    HYDROLASES)
                                                                                                                                                                                                                                                                                                                                                                SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                        linkages in cellulose.
                         CGACYTITCDTSQTKWCKPG-----GNSITITATNLCXPNWALPSNSGGWCN 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GPQDGFCAVWGCETTGETYWRPTSSWDYITVKKGVTQGIYQC-----SGGGWCGPCYD
CGQCIKLT----TTGGYVPGQGGPVREGLSKTFMITNLC-PN-IYPNQD--WCN
                                                       YNGKSCASTTNYHDSHKGACGCGPASGDAQFGWNA--GSFVAAASQMYFDSGNKGWCGQH
                                                                                  YGGKDGSCTMG-----GACGYGNL------YNAGYGLYNAALSSALFND-----GAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ITCDTSQTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMS--QPAWENIA 117
                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                      PS01140;
                                                                                                                                                                                                                                                                                    PSO1140; GLYCOSYL_HYDROL_F45; FALSE_NEG.
degradation; Hydrolase; Glycosidase.
24 NUCLEOPHILE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                     IPR000334; Glyco_hydro_45
                                                                                                                                                                        103
181 AA;
                                                                                                               Conservative
                                                                                                                                                                                                     132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          40, Created)
40, Last sequence update)
41, Last annotation update)
3.2.1.4) (Endo-1,4-beta-glucanase) (Cellulase)
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69
176
178
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                                                                                                                           7.1%;
32.5%;
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21.5%;
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                                                                                                               6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 85.5; [
Pred. No. 2.8;
                                                                                                                             Score 85; DB 1
Pred. No. 0.86;
                                                                                                                                                                                                                                                                            PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ----GASEGGRCNPLILQFTQKGRQTSWDG--
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                                                                                                               Mismatches
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                                                                                                                                           DB 1;
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                                                                                                                                        Length 181;
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EMBL; K01209; AAA43052.1; -
EMBL; V01172; CAA24497.1; -
EMBL; X001188; CAA25008.1; -
EMBL; M23026; -; NOT_ANNOTA
PIR; A03991; VCVWGF.
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CARBOHYD
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CONFLICT
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          CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      and GA-Fe
Virology
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Wunsch M., Schulz A.S., Koch W., Friedrich R., Hunsmann G.;
"Sequence analysis of Gardoner-Arnstein feline leukaemia virus
envelope gene reveals common structural properties of mammali
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Elder J.H., Mullins J.I.;
"Nucleotide sequence of the envelope leukemia virus B reveals unique seque mink cell focus forming virus.";
J. Virol. 46:871-880(1983).
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HSSP; P03385; 1MOF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Guilhot S., Hampe A., D'Auriol L., Galibert F. "Nucleotide sequence analysis of the LTRs and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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MEDLINE=83216322; PubMed=6304347;
                                 CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Nucleotide sequences of the envelope genes of two isolates of feline leukemia virus subgroup B.";
J. Virol. 49:629-632(1984).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ral envelope genes.";
2:2239-2246(1983).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       161:252-258(1987)
                                                                                                                                                                                                                                                                                                                              IPR002050; Env_polyprotein.
99
120
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158
                                                                           NOT_ANNOTATED_CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PubMed=2823466;
110
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63222
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SPIKE PROTEIN P15E.
R PROTEIN.
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N-LINKED (GLCNAC.
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N-LINKED (GLCNAC...
MISSING (IN REF. 4).
V -> I (IN REF. 4).
T -> V (IN REF. 4).
         NRKQ -> PSLGPKGTH (I
P -> A (IN REF. 4).
V -> A (IN REF. 4).
TYWRPT -> AWWKPS (IN
                                                                                                                                                                                                                                                                                                         Polyprotein; Signal.
                                                                                                                                                                                                      N-LINKED
N-LINKED
                                    IIGNTWAPSDQEPFPG -> LVGDSWEPIVLDPNNVAH
YSSSK (IN REF. 4).
DOPMRRRQORNT -> KTTDRKKQQOTY (IN REF.
NRKQ -> PSLGPKGTH (IN REF. 4).
                                                                          LVTGTK -> VQTNTQ (IN REF. 4).
FPTMYF -> YPTLHV (IN REF. 4).
IIGNTWNPSDQEPFPG -> LVGDSWEPI
                                                                                                                                                                                           N-LINKED
KGVTQGIYQCSGGGWCGPCYDKAVHSSTTGASEGGR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 elope gene of Gardner-Arnstein feline sequence homologies with a murine
                                                                                                                                (GLCNAC...)
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Best Local
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CARBOHYD
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                      CARBOHYD
CARBOHYD
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P03392;
                                                                                                                                                            CHAIN
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21-JUL-1986 (Rel. 01, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ENV polyprotein precursor (Coat polyprotein)
GP70; Spike protein P15E] (Fragment).
                                                                                                                                                                                                                                                                              EMBL; K01208; -; NOT_ANNOTATED_CDS. PIR; A03992; VCVWSF.
                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Viruses; Retroid
NCBI_TaxID=11780;
                                                             CARBOHYD
                                                                                                                                          CHAIN
                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                   Coat protein;
                                                                                                                                                                                                                       Pfam; PF00429; ENV_polyprotei
                                                                                                                                                                                                                                                              HSSP;
                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE=84115095; PubMed=6319767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                        InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jeukemia virus subgroup B.";
J. Virol. 49:629-632(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Nucleotide sequences of the envelope genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nunberg J.H., Williams M.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Feline sarcoma virus (strain Snyder-Theilen).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·! - PTM: SPECIFIC ENZYMATIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS
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                                                                                                                                                                                                                                                                                                                                                                                                                 s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VYQAGIVPVNYKRVPXQRSGGIRFAISGHDYFELVTVT
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                                                                                                                                                                                                                                                            P03385; 1MOF.
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TGSKVATQRPQTNESAPRSVAPTTMG (IN REF. 4).
; 1482088D547CFF47 CRC64;
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E PROTEIN P15E.
NKED (GLCNAC...
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01-MAY-1991 (Rel. 18, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
ENV polyprotein precursor (Contains: Coat protein GP70; Coat protein
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Nucleotide sequence and distinctive characteristics of the fendogenous feline leukemia provirus.";
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01-NOV-1995
16-OCT-2001
                                                                                                       Arnstein feline leukemia oncovirus B).
Viruses; Retroid viruses; Retroviridae
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                                                                                                                                                                                          Feline sarcoma virus (strain Gardner-Arnstein) (Ga-FeSV) (Gardner-
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"Nucleotide sequence and distinctive characteristics
of endogenous feline leukemia provirus.";
J. Virol. 63:2379-2384(1989).
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Viruses; Retroid viruses; Retroviridae; Gammaretrovirus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=89199802; PubMed=2539525;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P21444;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               213 -----PKSWGLRLYRSGYDPIALFSVS 234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               179 KAVHSSTT-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         60 ITCDTSQTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMS--QPAWENIA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14 GGKDGSCTMGGACGYGNLY----------NAGYGLYNAALSSALFNDGAMCGACYT 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 VYQAGIVPVNYKRVPXQRSGGIRFAISGHDYFELVTVT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPQDGFCAVWGCETTGETYWKPTSSWDYITVKKGVTQGIYQC-----SGGGWCGPCYD 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         P03390; 1AOL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR002050; Env_polyprotein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    273
273 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (Rel. 18, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            34
43
58
Williams M.E.,
                          PubMed=6319767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    >273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 20.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30008 MW; 6B605FCD582B325D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58
58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.28;
                                                                                                                                    Retroviridae; Gammaretrovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ------GASEGGRCNPLILQFTQKGRQTSWDG--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 86.5; DB Pred. No. 0.95;
Innis M.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      N-LINKED (GLCNAC. . .) (POTENTIAL).
N-LINKED (GLCNAC. . .) (POTENTIAL).
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P43213;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Poeae; Phleum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pollen allergen Phl p 1 precursor (Phl p I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
-i- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-i- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scheiner O., Duchene M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-95015525; PubMed-7930302;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE-Pollen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Phleum pratense (Common timothy)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       pROSITE; PS50843; EXPANSIN_CBD; 1.
pROSITE; PS50842; EXPANSIN_EG45; 1.
allergen; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P43214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X78813; CAA55390.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Complementary DNA cloning of the major allergen Phl p I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Laffer S., Valenta R., Vrtala S., Susani M., van
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000882; Pollen_allergen.
                                                                                                                                                                                                               102
                                                                                                                                                        118
205
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                                                                                                                                                                                                                                                                                                                  44
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                                                 NTG-WMAMSRNWGANWQSNA--YLAGQSLSFIVQ--LDDGRKVTAWNXAPXNW 219
                                                                                                                                                                                                               KPEACSGEPVVVHITDDN
                                                                                                                                                                                                                                                                                                                                                                       AFATFYGGKDGSCTM--GGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCDTS
GKDKWIELKESWGAIWRIDTPDKLTG---PFTVRYTTEGGTKTEAEDVIPEGW
                                                                                                      KLRSAGELELQFRRVKCKYPEGTKVTFHVEKGSNPNYLALL-VKYVNGDGDVVAVDIKEK
                                                                                                                                                                                                                                                              QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLX--HFDMSQPAWENIA-----
                                                                                                                                                                                                                                                                                                                  AKSTWYGKPTGAGPKDNGGACGYKDVDKPPFSGMTGCGNTPIFKSGRGCGSCFEIKC--T 101
                                                                                                                                                  -VYQAGIVPVNYKRVPXQRSGGIRFAI-----SGHDYFELVTVTNVGGSGVVAQMSIKGS 171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (Rel. 32, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24
61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1WHO.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                263
167
262
32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 12.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 152.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 POLLEN ALLERGEN PHL P
EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -LINKED (GLCNAC. . .) (
046BA249C17BC048 CRC64
                                                                                                                                                                                                                                                                                                                                                                                                                           ed. No. 1.30
Mismatches
                                                                                                                                                                                                               ----EEPIAPYHFDLSGHAFGAMAKKGDEQ 145
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Usage
                                                                                                                                                                                                                                                                                                                                                                                                                              95;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              43;
                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 8

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GUN5_TRIRE
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                                                                                                                                                                  Query Match
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15-DEC-1998 (Rel. 37, Last annotation update)
Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase (Cellulase V) (EG V).
                                                                                                                                                                                                                        CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Hypocreales; Hypo
NCBI_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GUN5_TRIRE P43317;
                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00734; CBD_1; 1.
Pfam; PF02015; Glyco_hydro_45; 1.
ProDom; PD001821; CBD_fungal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Trichoderma reesei (Hypocrea jecorina).
                                                                                                                                                                                                                                                                                                                                                                  PROSITE; PS00562; CBD_FUNGAL; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
PROSITE; PS01140; GLYCOSYL_HYDROL_F45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; Z33381; CAA83846.1; -. HSSP; P00725; 2CBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -!- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mol. Microbiol. 13:219-228(1994).
-i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   isolated by expression in yeast."; mol. Microbiol. 13:219-228(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saloheimo A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=95075308; PubMed=7984103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN=QM9414 / RUT C-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                           CHAIN
                                                                                                                                                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                                                                                                    Cellulose degradation; Hydrolase; Glycosidase; Signal
                                                                                                                                                                                                                                                                                                                                                                                                           SMART; SM00236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "A novel,
                                                                                                                                                                                                             DISULFID
                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                             ACT_SITE
                                                                                                                                                                                                                                                                                                           ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro;
                                                                                  16
                                                                                                                                                      Local
                          76 KCYQLT-STGQAPCSSCGTGGAAGQSIIVMVTNLC-PN----NGNAQWC--PVVGGTNQY 127
                                                                                                            3 SVAQSAFATFYGGKDGSCTMGGACG-YGNLYNAGYGLYNAALSSALFND------GAMCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HYDROLASES).
SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBU).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     linkages in cellulose
 ---XHFDM 108
                                                      ACYTITCDTSQT--KWCKPG---GNSITITATNLCXPNWALPSNSGGWCNPPL----
                                                                                  SAYKATTTRYYDGQEGACGCGSSSGAFPWQLGIGNGVYTAAGSQALFDTAGASWCGAGCG
                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A., Henrissat B., Hoffren A.-M., small endoglucanase gene, egl5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                IPR000254; CBD_fungal.
IPR000334; Glyco_hydrc
                                                                                                                                                                                                 242 AA;
                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hypocreaceae; Hypocrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                             fCBD;
                                                                                                                                                                                                                                       242
27
134
182
205
242
182
                                                                                                                                                                                                 24411 MW;
                                                                                                                                                        11.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               yco_hydro_45
                                                                                                                                           16;
                                                                                                                                                  CELLULOSE-BINDING (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL)
                                                                                                                                                                                                              BY SIMILARITY
                                                                                                                                                                                                                                                                    PRO/SER-RICH (LINKER)
                                                                                                                                                                                                                                                                                     CATALYTIC
                                                                                                                                                                                                                             BY SIMILARITY.
                                                                                                                                                                                                                                                                                               PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                           NUCLEOPHILE (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                              ENDOGLUCANASE V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                  CC033FC51326C71D CRC64;
                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        242 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            There are no restrictions on ong as its content is in no
                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from Trichoderma
                                                                                                                                            40;
                                                                                                                                                                     Length 242;
                                                                                                                                                                                                                                          .) (POTENTIAL).
                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Penttilae M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    reesei
                                                                                                                                            30;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local !
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; L14271; AAA33496.1; -. PIR; JC1524; JC1524. HSSP; P43214; IWHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene 131:227-230(1993).
-I- TISSUE SPECIFICITY: POLLEN TISSUE.
-I- DEVELOPMENTAL. STAGE: EXPRESSION LOW BEFORE AND HIGH AFTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PRO1225; EXPANSNPAMLY.
ProDom; PD002179; PO11en_allergen; 1.
PROSITE; PS50843; EXPANSIN_CBD; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Zea mays (Maize).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
enermaronhyta: Magnollophyta; Lilliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pollen allergen Zea m 1 (Zea m I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Allergen; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- DISEASE: CAUSES MAIZE POLLEN ALLERGY.
-!- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bedinger P.A.; "Zea mI, the maize homolog of the allergen-encoding Lol pI gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Broadwater A.H., Rubinstein A.L., Chay C.H., Klapper D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-94010312; PubMed-8406014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MPZ1_MAIZE
Q07154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MaizeDB; 65840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           rye grass.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TISSUE-Pollen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
168
                                                                                                                  109
                                                                                                                                                                             152
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                                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                        49
                                                                                                                                                                                                                                                                                                                                                                                                         47 LFNDGAMCGACYTITCDTSQTKWCKP--GGNSITITATNLCXPNWALPSNSGGWCNPPLX 104
                                                                                                                                                                                                                                                                                                                                                        9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POLLEN MITOSIS.
                                                                                                                                                                                                                                                                                                                                           IFKDGKGCGSCYEVRCKE-----KPECSGNPVTVFITDM---NY-----EPIA 48
                                                          VTAWNXAPXNW 219
                                                                                                                                                                    VTVTNVGGSGVVAQMSIKGS-NTGWMAMSRNWGANWQSNAYLAGQSLSFIVQL--DDGRK 208
                                                                                                                                                                                                                               PYHFDLSGKAFGSLAKPGLNDKLRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGCNPNYVA 108
                                                                                                                                                                                                                                                                                   --HFDMSQPAWENIA------VYQAGIVPVNYKRVPXQRSGG--IRFAISG--HDYFEL 151
VIAKDIIPANW 178
                                                                                                               VLVKFVADDGDIVLMEIQDKLSAEWKPMKLSWGAIWRMDTAKALKG-PFSIRLTSESGKK 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          105
191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          186 E
; 21362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13.2%; 27.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       32;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 157.5; DB 1; Length 191; Pred. No. 3.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXPANSIN-LIKE EG45. EXPANSIN-LIKE CBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          6E2A9DF921C45C63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          191 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             of
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PESULT 6

RESULT 7 MPP1_PHLPR

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Best Local
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16-OCT-2001 (Rel. 40, C
16-OCT-2001 (Rel. 40, L
01-MAR-2002 (Rel. 41, L
                                                                                                                                                                                                                                                                                              CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50843; EXPANSIN_CBD; 1. PROSITE; PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; S83343; AAB50734.2; -. HSSP; P43214; 1WHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cynodon dactylon (Bermuda grass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl.
Chloridoideae; Cynodonteae; Cynodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          _CYNDA
MPC1_CYNDA
                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                        Allergen.
                                                                                                                                                                                                                                                                                                                                                                                                ProDom; PD002179;
                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                            Pfam; PF01357; Pollen_allergen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Singh M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smith P.M., Suphioglu C., Griffith I.J., Therlault K., Knox R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96347957;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CYND1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=28909
   185
                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000882; Pollen_allergen.
                              174
                                                                                                                                                65
                                                                                                                   79
                                                                                                                                                                            21
                                                                                                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                         8
DEFIPMKSSWGAIWRIDPKKPLKG---PFSIRLTSEGGAHLVQDDVIPANW
                          G-WMAMSRNWGANWQSNAY--LAGQSLSFIVQL--DDGRKVTAWNXAPXNW 219
                                                        LRKAGELTLQFRRVKCKYPSGTKITFHIEKGSNDHYLALLVKYAAGDGNIVAVDIKPRDS
                                                                                    VYQAGIVPVNYKRVPXQRSGG--IRFAI--SGHDYFELVTVTNVGGSGVVAQMSIKGSNT
                                                                                                                KEPVEC--SGEPVLVKITDKNYEHIA-----AYHFDLSGKAFGAMAKKGQEDK 124
                                                                                                                                                                         ARATFYGSNPRGAAPDDHGGACGYKDVDKPPFDGMTACGNEPIFKDGLGCRACYETKC--
                                                                                                                                            SQTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIA-----
                                                                                                                                                                                                    AFATFYGGKDGSCT---MGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCDT
                                                                                                                                                                                                                                                                                                                                                                                                                PR01225; EXPANSNFAMLY
                                                                                                                                                                                                                                                                                              246 AA;
                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                          39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                  Pollen_allergen; 1. EXPANSIN_CBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PubMed=8757211;
                                                                                                                                                                                                                                                                                                                         145
240
                                                                                                                                                                                                                                                                                         145 EXPANSIN-LIKE EG45.
240 EXPANSIN-LIKE CBD.
9 N-LINKED (GLCNAC. . . ) (P-
26888 MW; 43D8442DBA588322 CRC64;
                                                                                                                                                                                                                                              13.1%;
25.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                                                                                                                     38;
                                                                                                                                                                                                                                Score 157; DB 1;
Pred. No. 4.8e-07;
B; Mismatches 96
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          246
                                                                                                                                                                                                                                                             DB 1; Length 246;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ş
                                                                                                                                                                                                                                                                                                          .) (POTENTIAL).
                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      biologically
grass pollen
                                                                                                                                                                                                                                   38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        pollen.";
                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       clade;
                                                        184
                                                                                                                                             117
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MPHL_HMALH MPHL_H MPHL_HMALH MPHL_HMALH MPHL_HMALH MPHL_HMALH MPHL_HMALH MPHL_HMALH MPHL_MMALH MALH MALH MPHL_MMALH MPHL_
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                        MPH1_HOLLA STANDARD;
P43216; Q39975;
01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last seq
01-MAR-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Cloning, expression and immunological characterization of Ory s the major allergen of rice pollen.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Xu H., Theer
Bhalla P.L.;
                                                    Spermatophyta; Magnoliophyta; Poeae; Holcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50843; EXPANSIN_CBD; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
Allergen; Glycoprotein; Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96069591; PubMed=7590339;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                        Holcus lanatus (Velvet grass).
Eukaryota; Viridiplantae; Stre
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U31771; AAA86533.1; -
                           NCBI_TaxID=29679
                                                                                                                                                                                        Major pollen allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000882; Pollen_allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 83
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADTKITFHIEKASNPNYLALL-VKYVAGDGDVVEVEIKEKGSEE-WKALKESWGAIWR 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGACGYKDVDKAPFLGMNSCGNDPIFKDGKGCGSCFEIKC--SKPEACSDKPALIHVTDM 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCDTSQTKWCKPGGNSITITAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GG--IRFAI---SGHDYFELVTVTNVGGSGVVAQMSI--KGSNTGWMAMSRNWGANWQ 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NLCXPNWALPSNSGGWCNPPLX--HFDMSQPAW----ENIAVYQAGIVPVNYKRVPXQRS 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P43214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Theerakulpisut P., Goulding N., Suphioglu C., Singh M.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              263 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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263
164
259
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13.7%;
29.8%;
                                                                                                                                                                                        Hol 1 1 precursor (Hol 1 I) (Hol 1 1.0101
                                                                                                                                                                                                                Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -DEPIAAYHFDLSGLAMAKDGKDEELRKAGIIDTQFRRVKCKYP 162
                                                                                  Streptophyta; Embryophyta; Tracheophyta;
yta; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 163.5; DB 1;
Pred. No. 1.4e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-LINKED (GLCNAC.
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MAJOR POLLEN ALLERGEN ORY S
EXPANSIN-LIKE EG45.

EXPANSIN-LIKE CBD.
                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B1C5F24EA398DD60 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                            265
                                                                                                                                                                                                                update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 263;
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                                                                                     Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          82
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schramm G.D., Bufe A., Petersen A., Haas H., Schlaak M., Becker "Mapping of IgE-binding epitopes on the recombinant major group allergen of velvet grass pollen, rHol 1 1.";
J. Allergy Clin. Immunol. 99:781-787(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CV. AVENEAE; TISSUE-Pollen;
Schramm G.D., Bufe A., Becker W.M., Schlaak M.;
Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           between the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There a use by non-profit institutions as long as i modified and this statement is not removed. Us
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=CV. AVENEAE; TISSUE=Poller
MEDLINE=96319506; PubMed=8768803;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                     proDom; PD002179; Pollen_allergen; 1.
pr0SITE; PS50843; EXPANSIN_CBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_aller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 18-265 FROM N.A
                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                              Allergen;
                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50842; EXPANSIN_EG45; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P43214; 1WHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000882; Pollen_allergen
                                                                                                             103
207 GKDKWIELKESWGAVWRVDTPDKLTG---PFTVRYTTEGGTKGEAEDVIPEGW
                                                                                                                                                                  46 AKSTWYGKPTGAGPKDNGGACGYKDVDKPPFSGMTGCGNTPIFKDGRGCGSCFEIKC---
                                                                                                                                                                                           8 AFATFYGGKDGSCTM--GGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCDTS
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                                                     KLRSAGELELKFRRVKCKYPDGTKPTFHVEKGSNPNYLALL-VKYIDGDGDVVAVDIKEK
                                                                              -VYQAGIVPVNYKRVPXQRSGGIR---FAI---SGHDYFELVTVTNVGGSGVVAQMSIKGS
                                                                                                             -TKPESCSGEPVTVHITD-----
                                                                                                                                     QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLX--HFDMSQPAWENIA-----
                          NTG-WMAMSRNWGANWQSNA--YLAGQSLSFIVQ--LDDGRKVTAWNXAPXNW
                                                                                                                                                                                                                                                                                                                                                                                                                                 PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Z27084; CAA81610.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Z68893; CAA93121.1; -.
                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                             Signal.
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                                                                                                                                                                                                                                                                             265 AA;
                                                                                                                                                                                                                       Conservative
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265
169
264
103
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                                                                                                                                                                                                                                                                                28590
                                                                                                                                                                                                                                    13.3%; score 159.5;
26.2%; Pred. No. 3.
                                                                                                                                                                                                                                                                                WW.
                                                                                                                                                                                                                        39;
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EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBJ.
T-> S (IN HOL L 1.0102).
T-> S (IN HOL CRC64;
                                                                                                             --DN----EEPIAPYHFDLSGHAFGSMAKKGEEQ
                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           There are no restrictions ong as its content is in
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                                                                                                                                                                                                                                                   DB 1;
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nbinant major group I
                                                                                                                                                                                                                          90;
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                                                                                                                                                                                                                           Indels 43;
                                                                                                                                                                                                                                                   Length 265;
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Best Local
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                                                                                                                                                                       01-NOV-1997
01-NOV-1997
01-MAR-2002
                                                                                                                                                                                                                                     _PHAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
CONFLICT
                                  MEDLINE-96105569; PubMed-8564724; Suphioglu C., Singh M.B.;
                                                                                                          Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poeae; Phalaris.
                                                                                                                          Phalaris aquatica (Canary grass).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                       01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Major pollen allergen Pha a 1 precursor (Pha a 1).
 pollen.
      "Cloning, sequencing and expression in Escherichia and four isoforms of Pha a 5, the major allergens c
                                                           TISSUE-Pollen
                                                                       SEQUENCE FROM N.A.
                                                                                                NCBI_TaxID=28479;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; M57474; AAA63279.1; -. EMBL; M57476; AAA63278.1; -. PIR; A23341; A23341.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                     206
                                                                                                                                                                                                                                                                                                      173 TG-WMAMSRNWGANWQSNA--YLAGQSLSFIVQ--LDDGRKVTAWNXAPXNW
                                                                                                                                                                                                                                                                                                                                                               118
                                                                                                                                                                                                                                                                                                                                                                                101 -TKPESCSGEAVTVTITD------DN-----EEPIAPYHFDLSGHAFGSMAKKGEEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro; IPR000882; Pollen_allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                66
                                                                                                                                                                                                                                                                                                                                                                                                                                      44
                                                                                                                                                                                                                                                                                                                                                                                                                                                               8
                                                                                                                                                                                                                       _PHAAQ
                                                                                                                                                                                                                                                                                 KDKWIELKESWGAVWRIDTPDKLTG---PFTVRYTTEGGTKSEFEDVIPEGW
                                                                                                                                                                                                                                                                                                                                                                                                                                 AKSTWYGKPTGAGPKDNGGACGYKNVDKAPFNGMTGCGNTPIFKDGRGCGSCFEIKC--- 100
                                                                                                                                                                                                                                                                                                                                 NVRSAGELELQFRRVKCKYPDDTKPTFHVEKASNPNYLAILVKYVDGDGDVVAVDIKEKG
                                                                                                                                                                                                                                                                                                                                                        -VYQAGIVPVNYKRV----PXQRSGGIRFAISGHDYFELVTVINVGGSGVVAQMSIKGSN 172
                                                                                                                                                                                                                                                                                                                                                                                                        QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLX--HFDMSQPAWENIA----- 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AFATFYGGKDGSCTM--GGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCDTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   S13614; S13614.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PS50843;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       263
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                                                                                                                                                                                                                       STANDARD;
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EXPANSIN_EG45; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 14.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Signal; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 172.5; DB Pred. No. 2.2e-08
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C V H G D
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EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC. .
      the major allergens of canary grass
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                                                                                                                                                                                                                       PRT;
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-> C (IN REF. 3).
-> WW (IN REF. 3).
7675896F279C88C9 CRC64;
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                                                                                                                   Poaceae;
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Best Local
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                                                                                 MPO1_ORYSA STAN
Q40638;
01-NOV-1997 (Rel. 3
01-NOV-1997 (Rel. 3
01-MAR-2002 (Rel. 4
      Major pollen allergen Ory s 1 precursor (Ory's 1).
Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trachcophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR01225; EXPANSNFAMLY.
PRODOM; PD002179; Pollen_allergen;
PROSITE; PS50843; EXPANSIN_CBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; S80654; AAB35984.1; -. HSSP; P43214; 1WHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -!- SUBCELLULAN LOCATION:
-!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
-!- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS
-!- SIMILARITY: COMMATNS 1 EXPANSIN-LIKE EG45 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Allergen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Suphioglu C., Singh M.B., Simpson R.J., Ward L., Knox R.B.;
"Identification of canary grass (Phalaris aquatica) pollen allergens
by immunoblotting: IgE and IgG antibody-binding studies.";
Allergy 48:273-281(1993).
-i- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                        211 GKDKWIELKESWGAIWRIDTPDKLTG---PFTVRYTTEGGTKAEFEDVIPEGW
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MEDLINE=93319091; PubMed=7687099;
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                                                                                                                                                                                                                                                                                                                                                                                                            AKSTWYGKPTGAGPKDNGGACGYKDVDKAPFNGMTGCGNTPIFKDGRGCGSCFELKC--S 107
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Last annotation update)
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P -> G (IN REF. 2).
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Title:
Perfect score:
Sequence:
Minimum DB seq length: 0 Maximum DB seq length: 2000000000
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2002 Compugen Ltd.
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database : SwissProt_40:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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## ALIGNMENTS

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"Isolation and characterization of a major cross-reactive grass group I allergenic determinant."; Mol. Immunol. 26:557-561(1989).  Mol. Immunol. 26:557-561(1989).  -i. SUBCELLULAR LOCATION: Secreted.  -i. DISEASE: CAUSES GRASS POLLEN ALLERGY.  -i. SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.  -i. SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOWAIN.  -i. SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.  -i. SIMILARI	rye-grass pollen."; FEBS Lett. 279:210-215(1991). [3] SEQUENCE OF 24-53. TISSUE-POLLEN; MEDLINE-86242068; PubMed-3718469; Cottam G.P., Moran D.M., Standring R.; "Physicochemical and immunochemical characterization of allergenic "physicochemical and immunochemical characterization of allergenic proteins from rye-grass (Lolium perenne) pollen prepared by a rapid and efficient purification method."; Biochem. J. 234:305-310(1986). [4] SEQUENCE OF 236-263. MEDLINE-88364850; PubMed-2475768;	Poeae; Lollum.  NCBL_TaxID=4522; [1] [1] [1] [1] [1] [2] [3] [3] [4] [5] [6] [7] [7] [8] [8] [8] [8] [8] [8] [8] [8] [8] [8	LT 1  LOLPR STANDARD; PRT; 263 AA.  MPLL_LOLPR STANDARD; PRT; 263 AA.  PL4946; P19964;  D1-APR-1990 (Rel. 14, Created)  O1-APR-1991 (Rel. 19, Last sequence update)  O1-MAR-2002 (Rel. 41, Last annotation update)  O1-MAR-7002 (Rel. 41, Last annotation update)  Tolium perenne Lol p 1 precursor (Lol p I) (Allergen R7).  Lolium perenne (Perennial ryegrass)  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae;

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RESULT 14
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                                                  MEDLINE-2137743; PubMed-1148525; Reldy B., McQueen-Mason S., Noesberger J., Fleming A.; "Differential Expression of alpha- and beta-expansin gelongating leaf of Festuca pratensis."; Plant Mol. Biol. 46:491-504(2001).

EMBL; AJ276006; CAC06432.1; -...
InterPro; IPR000882; Pollen_allergen.
PRINTS; PR01225; EXPANSNFAMLY.
PRODOM; PD002179; Pollen_allergen; 1.
SEQUENCE 253 AA; 26547 MW; BEB18079F6400A89 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Differential Expression of Expansin Genes Isolated from (Prunus avium L.) During Fruit Ripening.";
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF29752; AAG13983.1;
InterPro; IPR000882; Pollen_allergen.
Pfam; PF01325; POllen_allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
PRODOM; PD002179; Pollen_allergen; 1.
PRODOM; PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                      Festuca pratensis.
Eukaryota; Viridiplantae;
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01-DEC-2001
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Evantophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; Spermatophyta; Mosales; Rosaceae; Amygdaloideae; Prunus.
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                                                                                                                                                                                                      SEQUENCE FROM N.A.
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               Score 759.5;
Pred. No. 3.
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a; Poales; Poaceae; Pooidea
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Q9FY30;
01-MAR-2001
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"Differential Expression of alpha- and beta-expansin genes
elongating leaf of Festuca pratensis.";
Plant Mol. Biol. 46:491-594(2001).
EMBL; AJ276007; CAC06433.1; -.
InterPro; IPR000882; Pollen_allergen.
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PRODOM; PD002179; Pollen_allergen;
SEQUENCE 252 AA; 26544 MW; BE8
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Pred. No. 3.9e
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InterFor; IPR000882; POllen_allergen.
PRINTS; PR01225; EXPANSNEAMLY.
ProDom; PD002179; Pollen_allergen; 1.
                                                                                                                                                                    Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Etgu P., Lee Toriumi M., Yu G., Brooks S., Chao Q., Chen H., Karlin-Neumann G. Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Theologis A.; "Full Length cDNA of gene T20H2.4 (GI:8778980)."; Submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC02472; AAF79895.1; -. EMBL; AF33245; AAG48799.1; -. EMBL; AF33245; AAG48799.1; -. InterPro; IPR000882; Pollen_allergen.
                                                                                                                                                                                                                                                                                                                                                                            Sakano H., Vaysberg M., Lee J.M., Lenz C., Liu S., Pham P., Toriumi M., Yu G., Chin C., Chiou J., Choi E., Chung M., Gonzalez A., Howng B., Liu A., Altafi H., Brooks S., Buehler E., Chao Q., Conn L., Conway A.B., Hansen N.F., Johnson-Hopson C., Khan S., Kim C., Lam B., Miranda M., Nguyen M., Palm C.J., Shinn P., Southwick A., Davis R.W., Ecker J.R., Federspiel N.A., Theologis A., Theologis A.; "The sequence of BAC T20H2 from Arabidopsis thaliana chromosome 1.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidieurosids II; Brassicales; Brassicaceae; Arabidopsis.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
T20H2.4 PROTEIN (HYPOTHETICAL 26.8 KDA PROTEIN).
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ProDom; PD002179; Pollen_allergen; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      93 DPQWCKK-GVSVTITSTNFCPPNYNLPSNNGGWCNPPRPHFDMAQPAWEKIGIYKGGIVP
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                 VAQSAF-----ATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WQSNAYLDGQSISFKVTTSDGVTKTFLNIVPSSW 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WQSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VNYKRVPXORSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGAN 185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       138;
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                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           257 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COLUMBIA;
                                                                                                                       252 AA;
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                                                   Conservative
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                                                                                                                       26761 MW;
                                                                  63.9%;
21; Mismatches
                                                     27;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 765; DB 10;
Pred. No. 1.1e-62;
                                                                   Score 764.5; DB 1
Pred. No. 1.2e-62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
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                                                                                                                       9CE86DA49BEA931B CRC64;
                                                     Mismatches
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                                                                                     DB 10; Length 252;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             52;
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Q9FUM2

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Q9FUM2; Q9FUM2; 01-MAR-2001 01-MAR-2001

(TrEMBLrel. 16, (TrEMBLrel. 16,

Created)
Last sequence update)

PRELIMINARY;

PRT;

252

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RESULT

Q40636

ID 0636

AC 044

AC 04
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RESULT 13
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Pfam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
SEQUENCE 251 AA; 26826 MW; 29E99C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shcherban T.Y., Shi J., Durachko D.M., Guiltinan M.J., McQueen-Mason S.J., Shieh M., Cosgrove D.J., "Molecular cloning and sequence analysis of expansins--a highly conserved, multigene family of proteins that mediate cell wall extension in plants.";
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Q40636;
Q1-NOV-1996 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
EMBL; U30477; AAB38074.1; -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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01-DEC-2001 (Trem
EXPANSIN OS-EXP2
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                                                                                                                                                                                                                                                                                                                                                                         66 QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVP 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                       89 DGQWCLPG--SVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGIVP
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                                                                                                                                                                                                                                                                        VNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGAN 185
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                                                                                              WQSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGW 240
                                                                                                                                                      WQSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
                                                                                                                                                                                                                  VSYRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            63.7%; Score 762.5; DB 10; Length 251; 65.0%; Pred. No. 1.9e-62;
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Last annotation update)
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Q9ZP39
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Best Local
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
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01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
ALPHA-EXPANSIN PRECURSOR.
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MEDLINE-99026292; PubMed-9808735;
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                                                                                                                            Q-TKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIV 124
                                                                                                                                                                                                    QSAHATFYGGSDASGTMGGACGYGNLYSTGYGTNTAALSTALFNDGGSCGQCYKIMCDYN
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                                               PVNYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGA 184
  QDPKWCRK-GTYVTITATNFCPPNYALPSNNGGWCNPPRPHFDMAQPAWENIGIYRGGIV
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27754 MW;
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Q94KT5;
O1-DEC-2001 (TrEMBLrel. 19,
O1-DEC-2001 (TrEMBLrel. 19,
O1-DEC-2001 (TrEMBLrel. 19,
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SIGNAL
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Q9FVH0;
01-MAR-2001
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MEDLINE=21249159; PubMed=11351085;

Wu Y., Meeley R.B., Cosgrove D.J.;

"Analysis and Expression of the alpha-Expansin and beta-Expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
Panicoldeae; Andropogoneae; Zea.
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                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
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during Tomato Seed Germination.";
Plant Physiol. 124:1265-1274(2000)
                                               MEDLINE+20532800; PubMed=11080302;
Chen F., Bradford K.J.;
"Expression of an Expansin Is Associated with Endosperm
                                                                                                                                                                                                                                                                                                                   EXP8
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01-DEC-2001
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                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
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27775 MW;
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65.3%;
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Pred. No. 7
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7.5e-63;
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Best Local
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Shcherban T.Y., Shi J., Durachko D.M., Guiltinan M.J.,
McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
"Molecular cloning and sequence analysis of expansins--a highly
conserved, multigene family of proteins that mediate cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Q39625;
01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                   InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSHRAMLY.
PRODOM; PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                 extension in plants.";
Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
EMBL; U30382; AAB37746.1; -.
                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
STRAIN=BURPEE PICKLER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cucumis sativus (Cucumber).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Cucurbitales; Cucurbitaceae; Cucumis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AC007789; AAD38297.1; .
EMBL; AP002865; BAB18338.1; .
InterPro; IPR000882; Pollen_allergen.
Pfam; PP01357; Pollen_allergen; 1.
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PRODOM; PD002179; Pollen_allergen; 1
SEQUENCE 254 AA; 26987 MW; A4092
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DPKWCLPG--TIRVTATNFCPPNFALPNNNGGWCNPPLQHFDMAEPAFLQIAQYRAGIVP
                              QTKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVP 125
                                                                                QSAFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCDTS 65
                                                              QSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC-TN 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWWAMSRNWGANW 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SAFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCDTSQ 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QSNAYLTGQALSFRVQADDGGVVTAYDVAPANW 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RYARTPCRRVGGIRFGIAGHDYYELVLVTNVAGSGAVAAAWVKGSGTEWLSMSRNWGENW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVPV 126
                                                                                                                                            Similarity
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                                                                                                                              Conservative
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                                                                                                                                                                                         27215 MW;
                                                                                                                                           64.6%; Score 773.5; 64.5%; Pred. No. 1.8
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                                                                                                                         27; Mismatches
                                                                                                                                                                                                         EXPANSIN S1
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                                                                                                                           Indels
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RESULT 7
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Best Local
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Q946J1;
01-DEC-2001
01-DEC-2001
01-DEC-2001
                MEDLINE=21521099; PubMed=11641069; Lee Y., Choi D., Kende H.;
                                                                               Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsida Ehrhartoideae; Oryzeae; Oryzaa.
                                                                                                                         Oryza sativa (Rice).
                                                                                                                                         EXP2.
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Q94619;
                                                                                                                                                   ALPHA-EXPANSIN.
"Expansins: ever-expanding numbers
                                          SEQUENCE FROM N.A.
                                                                    NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Expansins: ever-expanding numbers and functions.", Curr. Opin. Plant Biol. 4:527-532(2001).
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01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21521099; PubMed=11641069; Lee Y., Choi D., Kende H.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                      141 IVPVNFQRVSCTRKGGVRFTINGNSYFELVLITNVGGPGSIKSVQIKGTKTGWVTMSRNW
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                                                                                                                                                                                                                                                                                                                                                                                                                                              22 AAALSGTATFYGGSDASGTMGGACGYGNLYSTGYGTNTAALSSALFNDGAACGECYQITC
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                                                                                                                                                                                                                                                                                                                                                                                           DQSNSKWCK-AGTSVTITATNLCPPDYSKPSNDGGWCNPPRQHFDMAQPAWEQIGVYRGG
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NCE 250 AA; 26429 MW;
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               Choi D., Kende H.
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63.1%;
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                                                                                             Liliopsida; Poales; Poaceae;
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  and functions.";
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                                                                                                         Embryophyta; Tracheophyta;
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                                                         RESULT 3
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Best Local
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SEQUENCE FROM N.A.
STRAIN=CV. NIPPONBARE;
Buell C.R., Benito M.-I., Lin X., Mason T.M., Umayam L.,
Fujii C.Y., Shen M., Fraser C.M.;
Fujii C.Y., Shen M., Fraser C.M.;
"Oryza sativa BAC T49920 genomic sequence.";
"Oryza sativa AC T49920 to the EMBL/GenBank/DDBJ databases.
้09FY29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases. EMBL; AC007789; AAD18326.1; ... EMBL; AC002865; BAB18336.1; ... InterPro; IPR000882; Pollen_allergen. Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1999 (TrEMBLrel.
01-NOV-1999 (TrEMBLrel.
01-JUN-2001 (TrEMBLrel.
PUTATIVE EXPANSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1
SEQUENCE 251 AA; 26334 MW; 1A0BB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Spermatophyta; Magnoliophyta; Liliopsida Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Oryza sativa nipponbare(GA3) genomic DNA, chromosome 1, clone:P0034C11.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T49B20.23 OR P0034C11.27. Oryza sativa (Rice).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03XHX0
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                                                                                                                                                               SNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
                                                                                                                                                                                                                                                                                                                                                        KWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVPVN 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                           AFATFYGGKDGSCTMGGACGYGNLYNAGYGLYNAALSSALFNDGAMCGACYTITCDTSQT
                                                                                                                                  SNARLDGQALSFRVQADDGRVVTAADVAPAGW
                                                                                                                                                                                                                                YRRVPCQRSGGIREAVNGHSYFELVLYTNVGGSGAVAQMWIKGSGTGWMAMSRNWGANWQ
                                                                                                                                                                                                                                                                               YKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGANWQ
                                                                                                                                                                                                                                                                                                                              QWCKP-GTSITVTATNFCPPNYALSGDAGGWCNPPRRHFDMSQPAWETIAVYRAGIVPVN
                                                                                                                                                                                                                                                                                                                                                                                                                                 AFATFYGGSDASGTMGGACGYGDLYGAGYGTRTAALSTALFNGGASCGACFTIACDTRKT 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NWGANWQSNAYLAGQSLSFIVQLDDGRKVTAWNVAPSNW 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 162;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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Last sequence update)
Last annotation update)
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Pred. No. 8.8e-74;
          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liliopsida; Poales;
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          255
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Best Local
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01-MAR-2001
01-MAR-2001
01-DEC-2001
EXPANSIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Reidy B., McQueen-Mason S., Noesberger J., Fleming A.;
"Differential Expression of alpha- and beta-expansin genes
elongating leaf of Festuca pratensis.";
plant Mol. Biol. 46:491-504(2001).
EMBL; AJ276008; CAC06434.1;
-InterPro; IPR000882; Pollen_allergen.
PRINTS; PR01225; EXPANSNFAMLY.
PRODOR; PD002179; Pollen_allergen; 1.
                                                                                                                                                                      STRAIN-CV. NIPPONBARE;
Buell C.R., Benito M. T., Lin X., Mason T.M.
Fujii C.Y., Shen M., Fraser C.M.;
"Oryza sativa BAC T49B20 genomic sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XHW9;
01-NOV-1999 (TrEMBLrel. 12,
01-NOV-1999 (TrEMBLrel. 12,
01-JUN-2001 (TrEMBLrel. 17,
                    STRAIN=CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yaman
"Oryza sativa nipponbare(GA3)
                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUTATIVE EXPANSIN.
T49B20.24 OR P0034C11.29.
       clone: P0034C11.";
                                                                                                        SEQUENCE
                                                                                                                                                  Submitted (JUN-1999)
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                              Oryza sativa (Rice).
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                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-21377433;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGANW
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159; Conserv
                                                                                                        FROM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE-ROOT
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16,
                                                                                                                                                    the
                                                    Yamamoto
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Last sequence up
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Last annotation update)
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                                                                                                                                                                                                                        Mason T.M.,
                          DNA,
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                          chromosome
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Gaps

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209

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Result
No.
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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Perfect score:
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                                                                                                                                                1173
885.5
866.5
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Gapop 10.0 , Gapext 0.5
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## ALIGNMENTS

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Local Similarity 73.6%;
nes 167; Conservative 2:
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Pred. No. 8.3e-95;
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                                                                                                                                                                                                                                                                                               Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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         99US-0121825
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22; Mismatches
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26-OCT-1999;
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28-OCT-1999;
28-OCT-1999;
29-OCT-1999;
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Local Similarity 73.6%;
nes 167; Conservative 2
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990S-0121825

990S-0125788

990S-0125788

990S-0126785

990S-0126785

990S-0127462

990S-0128714

990S-0128714

990S-0130077

990S-013047

990S-013048

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netic mapping; gene expression control;
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Pred. No. 7.8e
22; Mismatches
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les 29;
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              25-FEB-1999

05-MAR 1999

09-MAR 1999

23-MAR-1999

25-MAR-1999

20-APR-1999

01-APR-1999

16-APR-1999

16-APR-1999

21-APR-1999

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24-APR-1999

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26-MAY-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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RESULT 11
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16-JUN-1999
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                         63 VNDPQWCIKGRSIVVTATNFCPP-------GACDPNNHFDLSQPIYEKIALYKSGII 114
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76 ENDGKWCLPG-SIVVTATNFCPPNNALANNNGGWCNPPLEHFDLAQPVFQRIAQYRAGIV 134
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mes 167; Conserv
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; Pred. No. 7.5e-95;
22; Mismatches 29;
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hybridisation assay; genetic mapping; gene expression control; promoter;
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99US-0161406

99US-0161369

                                                                                                                      ; Score 927.5; DB 21;
; Pred. No. 7.5e-95;
22; Mismatches 29;
                                                                                                                                      21; Length
                                                                                                                        Indels
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                         194
                                       174
                                                                       114
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18-JUN 1999
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RESULT 8
AAG06546
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Best Local Similarity 99.5%;
Matches 200; Conservative
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20-SEP-1999;
22-SEP-1999;
23-SEP-1999;
24-SEP-1999;
24-SEP-1999;
29-SEP-1999;
29-SEP-1999;
20-CCT-1999;
20-CCT-1999;
21-CCT-1999;
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30-AUG-1999;
31-AUG-1999;
01-SEP-1999;
07-SEP-1999;
10-SEP-1999;
13-SEP-1999;
15-SEP-1999;
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9905-0161361
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Pred. No. le-113;
0; Mismatches
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119-APR-1999;
21-APR-1999;
23-APR-1999;
23-APR-1999;
23-APR-1999;
30-APR-1999;
30-APR-1999;
00-MAY-1999;
01-MAY-1999;
11-MAY-1999;
11-JUN-1999;
11-J
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05-MAR-1999

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01-APR-1999

06-APR-1999
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hybridisation assay; genetic mapping; gene expression control; promoter;
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99US-0123548.
99US-0125788.
99US-01264.
99US-01264.
99US-012824.
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99US-013286.
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990S-014259

990S-0142290

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990S-014220

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Best Local Similarity 99.8
Matches 200; Conservative
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13-SEP-1999;
15-SEP-1999;
16-SEP-1999;
20-SEP-1999;
23-SEP-1999;
24-SEP-1999;
24-SEP-1999;
28-SEP-1999;
29-SEP-1999;
04-OCT-1999;
   18-OCT-2000
                                        AAG51014 standard; Protein;
                     AAG51014;
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99US-0161361.
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99.5%;
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Pred. No. 1e-113;
0; Mismatches 1;
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  Protein identification; signal transduction pathway; metabolic hybridisation assay; genetic mapping; gene expression control;
                                Arabidopsis thaliana protein fragment SEQ ID NO: 16049.
                                                      17-OCT-2000
                                                                                               AAG15695 standard;
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nes 216; Conservative
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99US-0156458.
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99US-015695.
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99US-0160767.
99US-0160768.
99US-0160769.
99US-0161359.
99US-0161406.
99US-01614993.
99US-01614993.
                                                                                               Protein;
                                                     entry)
                                                                                                                                                                                                                                                                                                                      98.6%;
97.7%;
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Pred. No. 8.5e-124;
0; Mismatches 5;
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promoter;
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99US-0123180

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99US-0130077

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| 99US-0139763. 99US-0139817. 99US-0139899. 99US-0140353. 99US-0140354. 99US-0140695. 99US-0140823. 99US-0141287. 99US-0141287. 99US-0141842. 99US-0141842.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 99US-0139457.<br>99US-0139458.<br>99US-0139450.<br>99US-0139460.<br>99US-0139461.<br>99US-0139462.<br>99US-0139463.<br>99US-0139463. | 99US-0137724<br>99US-0138094<br>99US-0138540<br>99US-013847<br>99US-0139452<br>99US-0139452<br>99US-0139453<br>99US-0139454<br>99US-0139456                       | 99US-0134219<br>99US-0134270<br>99US-0134370<br>99US-0134768<br>99US-0135124<br>99US-0135533<br>99US-0135629<br>99US-0136392<br>99US-0136782<br>99US-0137528<br>99US-0137528                                                               | 99US-0130077. 99US-0130077. 99US-0130449. 99US-0130891. 99US-0131449. 99US-0132407. 99US-0132484. 99US-0132486. 99US-0132486. 99US-0132486. 99US-0132487. 99US-0132487. 99US-0132487.           | 2000EP-0301439. 99US-0121825. 99US-0123548. 99US-0125788. 99US-0126764. 99US-0126785. 99US-0128785. 99US-0128785. 99US-0128785.                                                                                                                                        |
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                  Arabidopsis thaliana
                                    Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Expansin proteins which alter the mechanical strength of poly:saccharide(s) - useful in paper mfr. and recycling
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                                                                                             hybridisation assay; genetic termination sequence.
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23-APR-1999;
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05-MAY-1999;
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14-MAY-1999;
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30-APR-1999;
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99US-0130510.
99US-0130891.
99US-0131449.
99US-0132048.
99US-0132407.
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99US-0127462.
99US-0128234.
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99US-0123180.
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99US-0126264
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s-0130077.
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RESULT 3
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AU9540262-A
                         Misc-difference
                                          Misc-difference
                                                          Misc-difference
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ches 217; Conserv
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YLNGQSLSEVVTTSDRRSVVSENVAPPTWSFGQTYTGGQFRY 255
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nilarity 97.7%;
Conservative
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Pred. No. 1.3e-124;
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99US-0145224.
99US-0145218.
99US-0147204.
99US-015404.
99US-015404.
99US-015404.
99US-015408.

18-AUG-1999
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RESULT 2
AAG51012
ID AAG5
XX AAG5
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XX AAG5
XX Arab
XX Prot
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KW term
XX Arab
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Best Local Similarity
Matches 217; Conserv
 25-FEB-1999;
05-MAR-1999;
09-MAR-1999;
23-MAR-1999;
25-MAR-1999;
29-MAR-1999;
01-APR-1999;
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                                                                                                                                                                                                                                                                              Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                 06-SEP-2000
                                                                                                                                                                                                                                                                                                                               Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                  AAG51012;
                                                                                                                                                                                                                                                                                                                                                                                                                               AAG51012 standard;
                                                                                                                                   25-FEB-2000;
                                                                                                                                                                                                                               Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                               thaliana protein fragment SEQ ID NO: 64702.
                                                                                                                                                                                                                                                               sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                   2000EP-0301439
990S-0121825.
990S-0123548.
990S-0125788.
990S-0125788.
990S-0126785.
990S-0127462.
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99US-0160767.
99US-0160770.
99US-0160814.
99US-0160815.
99US-0160980.
99US-0160980.
99US-0161404.
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99US-0161359.
99US-0161361.
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Pred. No. 1.3e
0; Mismatches
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| Arabidopsis        | AAG46484 | 21 | 207 |      | 790   | 44 |
| Arabidopsis        | AAG25444 | 21 | 207 | •    | 790   | 43 |
| Tomato seed expans | AAE00412 | 22 | 263 | •    | 796.5 | 42 |
|                    | AAG30324 | 21 | 257 | •    | 804.5 | 41 |
|                    | AAG30325 | 21 | 255 | 66.8 | 804.5 | 40 |
|                    | AAG36445 | 21 | 257 |      | 832.5 | 39 |
| Arabidopsis thalia | AAG46483 | 21 | 253 |      | 842   | 38 |
|                    | AAG25443 | 21 | 253 | •    | 842   | 37 |
|                    | AAG09620 | 21 | 280 | •    | 845.5 | 36 |
|                    | AAG09621 | 21 | 258 |      | 845.5 | 35 |
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| _                  | AAE00414 | 22 | 250 | 70.9 | 853.5 | ω  |
|                    | AAG29930 | 21 | 273 | •    | 855.5 | 32 |
|                    | AAG29931 | 21 | 262 | 71.1 | 855.5 | 31 |
| $_{r}$             | AAR94527 | 17 | 227 | •    | 857.5 | 30 |
|                    | AAG36568 | 21 | 255 | •    | 871.5 | 29 |
|                    | AAG36569 | 21 | 249 | •    | 871.5 | 28 |
|                    | AAG36570 | 21 | 242 |      | 871.5 | 27 |
|                    | AAG05451 | 21 | 255 |      | 876.5 | 26 |
|                    | AAG05452 | 21 | 249 | •    | 876.5 | 25 |
|                    | AAG05453 | 21 | 241 | 72.8 | 876.5 | 24 |
| منيز               | AAR94528 | 17 | 228 |      | 898.5 | 23 |
| Arabidopsis thal   | AAG23850 | 21 | 282 | •    | 907.5 | 22 |
| _                  | AAG43341 | 21 | 281 |      | 907.5 | 21 |
| S                  | AAG43342 | 21 | 253 | •    | 907.5 | 20 |
|                    | AAG23851 | 21 | 253 | •    | 907.5 | 19 |
| Arabidopsis tha    | AAG43343 | 21 | 251 | •    | 907.5 | 8  |
| S                  | AAG23852 | 21 | 251 | •    | 907.5 | 7  |
| Arabidopsis thal   | AAG51645 | 21 | 280 |      | 927.5 | 16 |
| S                  | AAG51631 | 21 | 259 | 77.0 | 927.5 | 5  |
| Arabidopsis thal   | 654      | 21 | 259 | 77.0 | 927.5 | 14 |
| Arabidopsis tha    | 5164     | 21 | 249 | •    | 927.5 | ω  |
| Arabidopsis tha    | AAG51632 | 21 | 249 | 77.0 | 927.5 | 2  |
|                    |          |    |     |      |       |    |

## ALIGNMENTS

RESULT 1 AAG15693

AAG15693 standard; Protein;

255

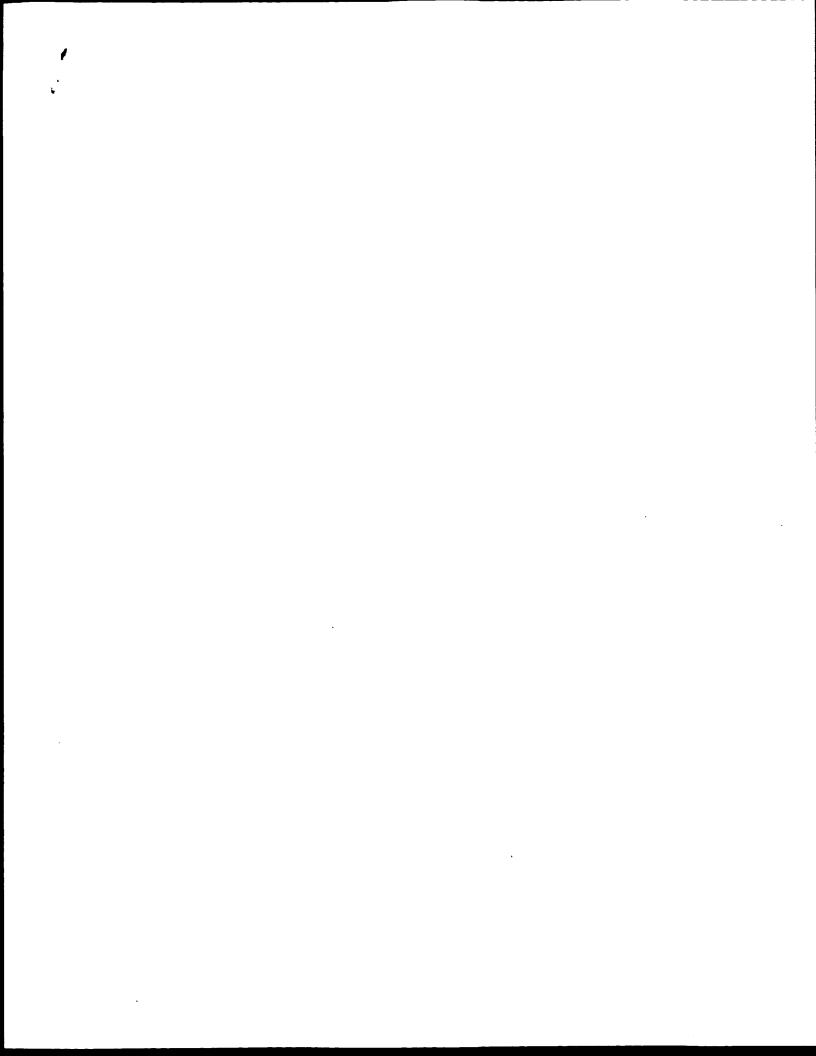
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17-OCT-2000 AAG15693;

(first entry)

25-FEB-1999 05-MAR-1999 09-MAR-1999 23-MAR-1999 25-MAR-1999 25-MAR-1999 01-APR-1999 01-APR-1999 16-APR-1999 16-APR-1999 19-APR-1999 11-APR-1999 21-APR-1999 Arabidopsis thaliana. Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; 06-SEP-2000. termination sequence Arabidopsis thaliana protein fragment SEQ ID NO: 16047. 25-FEB-2000; EP1033405-A2 2000EP-0301439 99US-0126264 99US-0126785 99US-0127462 99US-0128234 99US-01288714 99US-0129845 99US-0130077 99US-01300449 99US-0121825. 99US-0123180. 99US-0123548. 99US-0125788.

Arabidopsis



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RESULT 14
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FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
FEARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
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NUMBER OF SEQ ID NOS: 7
SOFTWARB: Patentin Ver. 2.1
SEQ ID NO 4
LENGTH: 227
TYPE: PRT
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APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: UNSURE LOCATION: (2)..(227) OTHER INFORMATION: X
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis OTHER INFORMATION: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                   187
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                                                                                    QSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTW 209
                                                                                                                                                                                                                                              POWCIK-GRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGIIPV 116
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                                                                 QSNAYLAGQSLSFIVQLDDGRKVTAWNXAPXNW 219
                                                                                                                                             NYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGANW
                                                                                                                                                                                MYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNW 176
                                                                                                                                                                                                                          TKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVPV 126
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57.7%; Pred. No. 7.3e-65;
mismatches 55;
                                                                                                                                                                                                                                                                                                                                                                                                                     Length 227;
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RESULT 15
US-09-362-642-6
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                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                Sequence 6, Application US/09362642 Patent No. 6350935
SOFTWARE:
SEQ ID NO 6
                                   APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ. ID NOS: 8
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Best Local Similarity
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APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Expansin Genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 6, Application US/08845539
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: protein
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
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MEDIUM TYPE: Floppy disk
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ZIP: 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/845,539
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0,
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CITY: San Francisco
STATE: California
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Best Local Similarity
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Patent No. 6350935
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APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
FILING DATE: 25-APR-1997
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bennett, Alan B.
APPLICANT: Rose, Jocelyn K.C.
TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
NUMBER OF SEQUENCES: 8
                                                                                                                                                                                                                    COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   211
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                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                            COUNTRY:
                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Joneson Eighth Floor
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REGISTRATION NUMBER:
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                                                                                                                                                                                                                                          94111-3834
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                                                                                                                                                                                                                                                                                    California
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              57.4%; Score 690.5; 63.6%; Pred. No. 1.6
                                                                                                US/08/845,539
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Mismatches 36
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -GGACDPPNHHFDLSQPIYEKIALYKS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 12
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    Matches 123;
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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                                                                                                                                          CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
APPLICANT:
                                                                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                      SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 225 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEPHONE: (415) 576-0300
TELEFAX: (415) 576-0300
                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        172 WGQNWQSNSYLNGQS 186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  151 GIVPVTYRRIPCRKQGGIRFTINGFRYFNLVLITNVAGAGDIIKVWVKGTKTNWIPLSRN 210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: NEC 28(
OPERATING SYSTEM:
                                                                                               TYPE:
                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                        APPLICATION NUMBER:
                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                               STATE:
                                                                                                                                                                                                                                                                                                                                                          STREET:
                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
                                                                               TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 TNTPNWKWCLPGNPSILITATNFCPPNYALPNDNGGWCNPPRPHFDLAMPMFLKLAQYRA 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           63 VNDP--QWCIKGR-SIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 GSWETAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGLSCGACFELKC
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                                                                                                            LENGTH:
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                                                                                            AMINO ACID
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    Conservative
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                                                                                                                                                                                                                                                                   FLOPPY DISK
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                   53.9%;
57.7%;
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63.6%;
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                                                                                                                                          4..
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    25;
Score 649; DB 4; Pred. No. 7.3e-65; Score 55;
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Pred. No. 2.7e-69;
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                               Length 227;
    Indels 10;
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    Gaps
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; OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis; OTHER INFORMATION: expansin US-09-092-160-6
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CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1993-05-12
VUMBER OF SEQ ID NOS: 7
CORTMANDE: DETAILS ON OF 1993-05-12
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Best Local Similarity
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SEQ ID NO 6
LENGTH: 226
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                                                                                    CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
APPLICANT: SHCHERBAN, TATYANA;
APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                         SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                 SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           177 QSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 220
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                65 DPOWCIKGRSIVVTATNFCPP------GGACDPNHHFDLSQPIYEKIALYKSGIIPV 116
                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
                                                                                                                                                                                                     COMPUTER: NEC 286
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                               CITY: UNIVERSITY PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 WQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTYLFNDGAACRSCYELRCDN 63
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TOPOLOGY:
          LENGTH: 222
THERE: AMINO ACID
                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                           COUNTRY:
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                                                                                                                                                                                                                                                                                                         UNITED STATES OF AMERICA
          UNKNOWN
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Pred. No. 2.5e-80;
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LENGTH: 225
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shicheban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                   Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/092,160C CURRENT FILING DATE: 1998-06-05
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NUMBER OF SEQ ID NOS: 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis OTHER INFORMATION: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        119 RRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRT-KWQLMSRNWGQNWQ 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             183 SNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     178 SNSYLNGQSLSFVVTTSDRRSVVSENVAPPTWSFGQTYTGGQF 220
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                                                                                                                        119 RRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRT-KWQLMSRNWGQNWQ 177
183 SNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEGGQF 225
                                        178 SNSYLNGQSLSEVVTTSDRRSVVSENVAPPTWSFGQTYTGGQF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELTC 62
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                                                                                                                                                                     63 EDDPEWCIPGSIIVRYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVPVAF 122
                                                                                                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                         63 VNDPQWCIKGRSIV-VTATNEC---PPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVMY 118
                                                                                                                                                                                                                                                      3 GGWERGHATFYGGADASGTMGGACGYGNLHSQGYGLQTAALSTALFNSGQKCGACFELTC 62
                                                                                                                                                                                                                                                                              3 GPWINAHATFYXXGDAXXIMGGACGYGNLYSOGYGLETAALSTALFDOGLSCGACXELMC 62
                                                                                  143;
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                                                                                                                                                                                                                                                                                                                                                               64.6%; Score 777.5; DB 4 64.1%; Pred. No. 2.9e-79;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 227
TYPE: PRT
                                                                                                                                                                                                                                                      Matches 152; Conservative
                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/ICI14US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/092,160C CURRENT FILING DATE: 1998-06-05
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                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: expansin
                                                                                                                                                                                                                                                                                                                                                                                                          FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: UNSURE LOCATION: 211
63 TNDPKWCLPG-TIRVTATNFCPPNFALPNDDGGWCNPPLQHFDMAEPAFLQIAQYRAGIV 121
                                                                                                                        63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         182
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122 PVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  115 PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                                                                                                                                                                         Match 71.2%;
Local Similarity 67.3%;
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                                                                                                                                                                                                       3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC 62
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                                                                                                                                                                GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Application US/09092160C
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                                                                                                                                                                                                                                                      26; Mismatches
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                                                                                                                                                                                                                                                                       Score 857.5; DB 4
Pred. No. 3.2e-88;
                                                                                                                                                                                                                                                                                         DB 4; Length 227;
                                                                                                                                                                                                                                                  39; Indels 9; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                             Matches 146;
                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 6, Approximately No. 5959082
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
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                                                                     183 QSNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEGGQF 226
                                                                                                          177 QSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 220
                                                                                                                                               123 SYRRYPCVKKGGIRFTINGHSYFNLVLYTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQNW 182
                                                                                                                                                                                    117 MYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNW 176
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                                                                                                                                                                                                                           64 DGQWCLPG-SYTYTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGIVPV 122
                                                                                                                                                                                                                                                                  65 DPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGIIPV 116
                                                                                                                                                                                                                                                                                                                                                                                                     Match 65.4%; Score 787; DB 2; Length 226; Local Similarity 65.2%; Pred. No. 2.5e-80;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            182 NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: NEC 280
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/440,517A FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: 113 TECHNOLOGY CITY: UNIVERSITY PARK
                                                                                                                                                                                                                                                                                                       5 WQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYELRCDN 63
                                                                                                                                                                                                                                                                                                                             5 WINAHATEYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALEDQGLSCGACXELMCVN 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: INTELLECTUAL PROPERTY OFFICE,
ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
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                                                                                                                                                                                                                                                                                                                                                                                           Conservative 21; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      UNITED STATES OF AMERICA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GUILTINAN, MARK;
SHCHERBAN, TATYANA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNKNOWN
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APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: McQueen-Mason, Simon
APPLICANT: Shitinan, Mark J
APPLICANT: Shit, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3

GENERAL INFORMATION:

Sequence 6, Application US/09092160C Patent No. 6255466

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                                                                                                                                                                      Sequence 2, Application US/08440517A Patent No. 5959082
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SEQ ID NO 3
LENGTH: 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                              GENERAL INFORMATION:
APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
APPLICANT: SHCHERBAN, TATYANA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
RUMBER OF SEQ ID NOS: 7
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APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/092,160C CURRENT FILING DATE: 1998-06-05
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LOCATION: (14)..(58)
OTHER INFORMATION: Xaa is unknown or other
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                        APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                              181 YLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFRY 222
                                                                                                                                                                                                                                                                                                                    181 YLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFRY 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 MCVNDPQWCIKGRSIVVTATNFCPPGGACDPNHHFDLSQPIYEKIALYKSGIIPVMYRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity
les 222; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               VRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNS 180
                                                                                                                                                                                                                                                                                                                                                                               VRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MCVNDPQWCIKGRSIVVTATNFCPPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVMYRR 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
APPLICANT: COSGROVE, Daniel J
APPLICANT: MCQUEEN-MASON, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
                                                                             SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2,
                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER APPLICATION NUMBER: 08/260,944
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No. 6255466
                                                                                                                                              EARLIER FILING DATE: 1993-05-12 NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
OTHER INFORMATION: Description of Artificial Sequence: rice expansin
                       FEATURE:
                                      ORGANISM: Artificial Sequence
                                                                  TYPE: PRT
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/440,517A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: UNKNOWN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NWQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTGAHVR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NWQSNSYLNGQSLSEVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNDGKWCLPG-SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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Pred. No. 8.2e-93;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 228;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      9;
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FEATURE:

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Minimum DB seq length: Maximum DB seq length:
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Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
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US-08-175-096-4
US-08-173-288-6
US-08-441-507-21
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Compugen Ltd.
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          121
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Result No.

## ALIGNMENTS

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Sequence 3, Application US/08440517A Patent No. 5959082
                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: COSGROVE,
APPLICANT: GUTLITINAN,
APPLICANT: SHCHERBAN
APPLICANT: SHI, JUN
TITLE OF INVENTION: F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: UNITED STAT ZIP: 16802-7000 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 6
                   121 VRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: INTELLECTUAL PROPERTY OFFICE,
ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
STREET: 113 TECHNOLOGY CENTER
CITY: UNIVERSITY PARK
STATE: PENNSYLVANIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: NEC 286
OPERATING SYSTEM:
                                                                            61 MCVNDPQWCIKGRSIVVTATNFCPPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVMYRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                              1 HMGPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXEL
                                                                                                                                                                                 1 HMGPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXEL
VRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNS
                                                                                                  MCVNDPQWCIKGRSIVVTATNFCPPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVMYRk 120
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SHCHERBAN, TATYANA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COSGROVE, DANIEL J.;
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100.0%; Pr
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Pred. No. 6.1e-126;
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60 60

180 120

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CURRENT FILING DATE: 1998-05-01
EARLIER APPLICATION NUMBER: 60/04
EARLIER FILING DATE: 1997-05-02
NUMBER OF SEQ ID NOS: 37
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 37
LENGTH: 254
TYPE: PRT
ORGANISM: Arabidopsis
US-09-071-252-37
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                                                                                                                                                                                                                                                                                                              : OTHER INFORMATION: xaa is any amino acid
NAME/KEY: misc_feature
: LOCATION: 1..25
: LOCATION: 1..25
: OTHER INFORMATION: Ceres Seq. ID 1842533
US-09-708-427-35961
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US-09-708-427-35961
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 35961
LENGTH: 235
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 35961, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 163; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ouery Match 75.5%; Score 909.5; DB 14; Length 254; Best Local Similarity 73.1%; Pred. No. 8.2e-89; Matches 166; Conservative 19; Mismatches 33; Indels 9;
                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature LOCATION: 1..235
                                                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Arabidopsis thaliana
117 MYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNW 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     148
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                                                                              12 WVNAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIKCQS 71
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72.48;
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Pred. No. 1.2e-88;
24; Mismatches 29;
                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                       Length 235;
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Search completed: October 11, 2002, 15:12:21 Job time: 99.6303 secs

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В
                             Qy
                                                                                                                                            ; FEATURE:
US-60-324-109-21386
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 12
                                                                                                                                                                                                         APPLICANT: Stein, Joshua
TITLE OF INVENTION: cDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
SEQ ID NO 21386
LENGTH: 264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/595,329A
CURRENT FILING DATE: 2000-66-16
NUMBER OF SEQ ID NOS: 3309
SOFTWARE: Patentin version 3.0
SEQ ID NO 2001
                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 21386, Application US/60324109 GENERAL INFORMATION:
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APPLICANT: ALEXANDROV, Nickoli
APPLICANT: VYACHESLAV, Brover
TITLE OF INVENTION: Sequence:
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-0948P
                                                                                      Query Match
Best Local :
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APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: peptide
LOCATION: (1)..(260)
OTHER INFORMATION: Ceres
                                                                                                                                                                                                 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Arabidopsis Thaliana
                                                                                                                                                                           ORGANISM: Glycine max
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      213 NWQSNSYLNGQALSFKVTTSDGRTVVSFNAAPAGWSYGQTFAGGQFR 259
 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94 ENDGKWCLPG-SIVYTATNFCPPNNALANNNGGWCNPPLEHFDLAQPVFQRIAQYRAGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 114
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                                 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PVSYRRVPCRRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAAIKGSRTVWQAMSRNWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGWINAHATFYGGGDASGTMGGACGYGNLYSQGYGTSTAALSTALFNNGLSCGSCFEIRC
                                                                      167;
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                                                                                      Similarity
                                                                      Conservative
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73.6%;
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73.6%;
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                                                                      19;
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                                                                    Score 913.5; DB 26; Pred. No. 3.2e-89; 9; Mismatches 32;
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                                                                                                       DB 26;
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US-09-112-498A-7
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                                                                            Sequence 37, Application US/09071252C GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence 7, Application US/09112498A
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 166;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
APPLICANT: Cosgrove, Daniel J
TITLE OF INVENTION: BETA-EXPANSINS AS CELL WALL LOOSENING
TITLE OF INVENTION: COMPOSITIONS THEREOF AND METHODS OF US
FILE REFERENCE: 11940E183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 11-JUL-19
INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                       131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY:
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                                                                                                                                                                                                                                                                                                                                                                                                                       12 GGWYNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC
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                                                                                                                                                                                          NWQSNSYLNGQSLSFKVTTSDGQTIVSNNVANAGWSFGQTFTGAQLR 237
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                                                                                                                                                                                                                              NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                       PVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQ 190
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CURRENT APPLICATION NUMBER: US/09/071,252C

AGENTS,

US-09-570-581A-1823

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TYPE: PRT
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NAME/KEY: peptide

LOCATION: (1)..(242)

OTHER INFORMATION: Ceres Seq. ID no. 1015119

NAME/KEY: misc_feature

LOCATION: ()..()

OTHER INFORMATION: Xaa is any aa, unknown or other

US-09-595-329A-2003
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                                 CURRENT APPLICATION NUMBER: US/09/570,581A CURRENT FILING DATE: 2001-05-12 NUMBER OF SEQ ID NOS: 1950 SOFTWARE: PATENTIN VERSION 3.0 SEQ ID NO 1823 LENGTH: 249
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                                                                                                                               TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides TITLE OF INVENTION: Thereby FILE REFERENCE: 2750-0875by
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SEQ ID NO 2003
ORGANISM: Arabidopsis thaliana
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APPLICANT: VYACHESLAV, Brover
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Sequence 2001, Application US/09595329A
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LENGTH: 250
TYPE: PRT
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LOCATION: ()...()
OTHER INFORMATION: Xaa is any aa, unknown or other
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LOCATION: (1)..(250)
OTHER INFORMATION: C
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                                                                                  203 NWQSNSYLNGQALSFKVTTSDGRTVVSFNAAPAGWSYGQTFAGGQFR 249
                                                                                                      175 NWOSNSYLNGOSLSEVVTTSDRRSVVSENVAPPTWSEGOTYTGGOER 221
                                                                                                                                                        143 PVSYRRVPCRRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAAIKGSRTVWQAMSRNWGQ 202
                                                                                                                                                                                        115 PVMYRRVRCKRSGGIRFTINGHSVENLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
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LENGTH: 221
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APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
TITLE OF INVENTION: Thereby
FILE REFERENCE: 2750-1067P
CURRENT APPLICATION NUMBER: US/09/620,394B
CURRENT FILING DATE: 2000-07-21
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                       Sequence 4044, Application US/09620394B GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 9131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1. 221
OTHER INFORMATION: xaa is any amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 1..221
OTHER INFORMATION: Ceres Seq. ID 1388406
        APPLICANT: ALEXANDROV, Nickolai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          181 YLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFRY 222
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 HMGPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXEL 60
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                                                                                                                                                                                  121 RCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNSY 180
                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity
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                                                                                                                                                                                                                                                              62 CVNDPQWCIKGRSIVYTATNFCPPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVMYRRV 121
                                                                                                                                                                                                                                                                                                          1 MGPWINAHATFYGGGDASGTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACFELM 60
                                                                                                                                                                                                                                                                                                                                        2 MGPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELM 61
                                                                                                                                                                                                                                              CVNDPQWCIKGRSIVVTATNFCPPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVMYRRV 120
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BROVER, Vyachesiav
                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                          98.6%; Score 1187; DB 20; 97.7%; Pred. No. 9.9e-119;
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 221;
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US-09-620-394B-4044
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                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Cao, Yongwei
APPLICANT: Edgerton, Michael D
APPLICANT: Hinkle, Gregory J.
APPLICANT: Kovalic, David K.
APPLICANT: Liu, Jingdong
APPLICANT: Stein, Joshua
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     sequence 21420, Application US/60324109
                                                                                                                                                                                                                                                                                                     SEQ ID NO 21420
                                                                                                                                        Matches 176; Conservative
                                                                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT FILE REFERENCE: 38-10(52726)B
CURRENT APPLICATION NUMBER: US/60/324,109
CURRENT FILING DATE: 2001-09-21
NUMBER OF SEQ ID NOS: 33196
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LOCATION: 1..201
OTHER INFORMATION: Ceres Seq. ID 1388407
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME/KEY: misc_feature
                                                                                                                                                                                                                                                  ORGANISM: Glycine max
                                                                                                                                                                                                                                   FEATURE:
                                                                                                                                                                                                                                                                     TYPE: PRT
                                                                                                                                                                                                                                                                                    LENGTH: 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   142 VLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNSYLNGQSLSFVVTTSDRKSVVS 201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 91.0%;
Local Similarity 99.5%;
63 VNDPQWCIKGRSIVVTATNFCPPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVMYRRVR 122
                                                                    29 GGWTNAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGSCYQIKC 88
                                                                                                    3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC 62
                                                                                                                                                               Local
                                                                                                                                                           h 83.4%; Score 1004.5; DB 26; Length 247; Similarity 80.0%; Pred. No. 4.8e-99;
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                                                                                                                                                 22; Mismatches
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Pred. No. 5.4e-109;
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Sequence 4042, Application US/09620394B
GENERAL INFORMATION:
APPLICANT: ALEXANDROV, Nickolai
APPLICANT: BROVER, Vyacheslav
TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 9, Application:
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches 217;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/893,766 FILING DATE: 11-JUL-1997 INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: FITTLE OF INVENTION: FITTLE OF INVENTION: SUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 233 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT
                                                                                                                                                                       192
                                                                                                                                                                                                                                 132 VRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNS 191
                                                                                                                                                                                                 181 YLNGQSLSEVVTTSDRRSVVSENVAPPTWSEGQTYTGGQFRY 222
                                                                                                                                                                                                                                                     121 VRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNS 180
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                                                                                                                                                                                                                                                                                                                72
                                                                                                                                                                                                                                                                                                                         61 MCVNDPQWCIKGRSIVVTATNFCPPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVNYRR 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                YLNGQSLSEVVTTSDRRSVVSENVAPPTWSFGQTYTGGQFRY 233
                                                                                                                                                                                                                                                                                                         MCVNDPQWCIKGRSIVVTATNECPPGGACDPPNHHEDLSQPIYEKIALYKSGIIPVMYRR 131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.38;
97.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MICROBIAL SWOLLENIN PROTEIN, DNA SEQUENCES ENCODING SUCH SWOLLENINS AND METHOD OF PRODUCING SWOLLENINS
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Pred. No. 1.5e-119;
0; M1smatches 5;
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; OTHER INFORMATION: Description of Artificial Sequence: NAME/KEY: UNSURE ; LOCATION: (14)..(58) ; OTHER INFORMATION: Xaa is unknown or other. US-09-896-301-3
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APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltlanan, Mark J
APPLICANT: Shicherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/896,301
CURRENT APPLICATION NUMBER: 09/092,160
PRIOR APPLICATION NUMBER: 09/092,160
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 08/440,517
PRIOR FILING DATE: 1998-05-12
PRIOR FILING DATE: 1995-05-12
PRIOR FILING DATE: 1995-05-12
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; LOCATION: 1..255
; OTHER INFORMATION: Ceres Seq. ID 1388405
US-09-620-394B-4042
                                                                                                                                                                                                     SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09896301 GENERAL INFORMATION:
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CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9131
SEQ ID NO 4042
                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 08/242,090
PRIOR FILING DATE: 1994-05-12
PRIOR APPLICATION NUMBER: 08/060,944
PRIOR FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
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Best Local
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                                                                                                              LENGTH: 222
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
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NAME/KEY: misc_feature
LOCATION: 1. 255
OTHER INFORMATION: Xaa is any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNS
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97.7%;
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Pred. No. 1.6e-119;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Title:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   October 11, 2002, 14:56:50 ; Search time 98.6303 Seconds (without alignments) 792.249 Million cell updates/sec
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Listing first 45 summaries
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Copyright (c) 1993 - 2002 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/2/paa/US06_COMB.pep:*
/cgn2_6/ptodata/2/paa/US07_COMB.pep:*
/cgn2_6/ptodata/2/paa/US080_COMB.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /cgn2_6/ptodata/2/paa/PCTUS_COMB.pep:*
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/cgn2_6/ptodata/2/paa/US096_COMB.pep:*
/cgn2_6/ptodata/2/paa/US097_COMB.pep:*
/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
/cgn2_6/ptodata/2/paa/US099_COMB.pep:*
/cgn2_6/ptodata/2/paa/US100_COMB.pep:*
/cgn2_6/ptodata/2/paa/US101_COMB.pep:*
/cgn2_6/ptodata/2/paa/US60_COMB.pep:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| NO.          | Score<br>1195 | Ouery Match Length DB 99.3 233 15 | Length<br>233 |    | ID<br>5 US-09-112-498-10<br>5 IIS-09-112-098A-9 | Description Sequence 10, Appl Sequence 9, Appli |
|--------------|---------------|-----------------------------------|---------------|----|-------------------------------------------------|-------------------------------------------------|
| _            | 1195          | 99.3                              |               | 15 | US-09-112-498-10                                | Sequence 10, App                                |
| N            | 1195          | 99.3                              | 233           | 15 | US-09-112-498A-9                                | Sequence 9, App                                 |
| ω            | 1195          | 99.3                              | 255           | 20 | US-09-620-394B-4042                             | Sequence 4042,                                  |
| 4            | 1194          | 99.2                              | 222           | 22 | US-09-896-301-3                                 | Sequence 3, App                                 |
| <sub>5</sub> | 1187          | 98.6                              | 221           | 20 | US-09-620-394B-4043                             | Sequence 4043, 1                                |
| σ            | 1096          | 91.0                              | 201           | 20 | US-09-620-394B-4044                             | Sequence 4044,                                  |
| 7            | 1004.5        | 83.4                              | 247           | 26 | US-60-324-109-21420                             | Sequence 21420,                                 |

| 45      | 44           | 43             | 42              | 41             | 40             | 39               | 38           | 37              | 36             | ω<br>5        | 34            | ယ       | 3<br>2          | 31           | 30         | 29            | 28            | 27            | 26             | 25             | 24               | 23             | 22           | 21          | 20           | 19                | Д<br>8          | 17              | 16               | 15            | 14             | 13          | 12               | 11               | 10               | 9                | 89              |
|---------|--------------|----------------|-----------------|----------------|----------------|------------------|--------------|-----------------|----------------|---------------|---------------|---------|-----------------|--------------|------------|---------------|---------------|---------------|----------------|----------------|------------------|----------------|--------------|-------------|--------------|-------------------|-----------------|-----------------|------------------|---------------|----------------|-------------|------------------|------------------|------------------|------------------|-----------------|
|         | 27           | 28             | 32              | 32.            | 32.            |                  | 41.          | 4               |                |               |               |         |                 |              |            |               |               |               |                |                |                  |                |              |             |              |                   |                 |                 |                  |               |                |             |                  |                  |                  |                  |                 |
| 68.4    | œ            | œ              | 9               | 9              | 9              | 9                | 9            | 9               | 0              | 0             | 0             | 0       | _               | _            | _          | _             | 2             | 2             | 2              | 2              | 2                | 4.             | 4            | 4           |              | 5                 | 5               | 5               | 5                | 5             | 5              | 5           | .5               | .7               | 7.               | .7               | 7.              |
| 232     |              |                |                 |                |                |                  |              |                 |                |               |               |         |                 |              |            |               |               |               |                |                |                  |                |              |             |              |                   |                 |                 |                  |               |                |             |                  |                  |                  |                  |                 |
| 15      | 15           | 19             | 15              | 21             | 15             | 26               | 21           | 20              | 14             | 14            |               |         |                 |              |            |               | 26            | 15            | 19             | 19             | 19               | 15             | 15           | 15          | 22           | 19                | 19              | 26              | 21               | 21            | 14             | 15          | 26               | 19               | 19               | 19               | 19              |
| 09-112- | -09-112-498- | -09-595-329A-9 | -09-112-498A-13 | -09-708-427-20 | -09-112-498-14 | -60-324-109-2297 | -09-708-427- | -09-689-980-152 | -09-071-252-22 | -09-071-252-2 | -09-410-191-6 | S00-268 | -09-708-427-175 | -09-708-427- | -09-896-3  | -09-112-498A- | -60-324-109-2 | -09-112-498-5 | 9-595-328C-191 | -09-595-328C-1 | -09-595-328C-191 | -09-112-498A-3 | -09-112-498- | -09-112-498 | -09-896-301- | 9-595-329A-95     | -09-595-329A-95 | -60-312-544-660 | -09-708-427-3596 | -09-708-427-3 | -09-071-252-37 | 9-112-498A- | -60-324-109-2138 | -09-595-329A-200 | -09-595-329A-200 | -09-570-581A-182 | 9-595-329A-2    |
| 8, Appl | e 6, Appl    | 956, Ap        | 13, App         | 2083, A        | 14, App        | 229/6,           | 9695         | 152, Ap         | 22, App        | 23            | 6,            | 6, 2    | 1756,           | equence 175  | equence 7, | e<br>5,       | equence 226   | equence 5,    | equence 191    | equence 191    | 15               | ω              | 4,           | 8           | N            | Sequence 954, App | 955             | 660             | 35960,           | 35961,        | ddv            | 7, Appl     | e 21386,         | e 2001, A        | e 2002,          | equence 1823, A  | equence 2003, A |

## ALIGNMENTS

; Sequence 10, Application US/09112498; GENERAL INFORMATION:

RESULT 1 US-09-112-498-10

- Вb Q
- Q В

Search completed: October 11, 2002, 15:15:44 Job time: 31.293 secs

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RESULT 14
US-09-935-625-31515
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US-09-935-625-23153
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: POLYNUCLEOTIDES, POLYN
TITLE OF INVENTION: MODULATING VARIOUS REFILE REFERENCE: 2750-1481P
CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 23153
LENGTH: 250
                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 23153, Application US/09935625 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: peptide
LOCATION: 1..250
OTHER INFORMATION: Ceres
                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Ceres Seq. ID no. 3446951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: peptide LOCATION: 1..250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Arabidopsis
                                                             204
                                                                                        175 NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                      115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           204 NWQSNSYLNGQSLSFKVTTSDGQTIVSNNVANAGWSFGQTFTGAQLR 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   115
                                                                                                                                                                                                               63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 114
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                                                                                                                                                                                                                                                                          3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC
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                                                                                                                                   PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
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                                                                                                                                                                                   QNDGKWCLPG-SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV 143
                                                                                                                                                                                                                                             GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC 84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC
                                                                                                                                                                                                                                                                                                           166;
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73.1%;
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73.1%;
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                                                                                                                                                                                                                                                                                                         19;
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                                                                                                                                                                                                                                                                                                                      Score 909.5; DB 5
Pred. No. 7.6e-88;
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Pred. No. 7.6e-88;
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QNDGKWCLPG-SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV 143

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CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 31519
LENGTH: 250
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                        Matches
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                                                                                                                                     Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: N. ALEXANDROV et al.
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CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                            ORGANISM: Arabidopsis FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: PRT ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                        NAME/KEY: peptide
LOCATION: 1..250
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63 VNDPQWCIKGRSIVVTATNFCPP-----
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                                                                                                                         Local Similarity
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                                  GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC 84
                                                                  GPWINAHATEYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALEDQGLSCGACXELMC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNDGKWCLPG-SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAG1V-143
                                                                                                        166;
                                                                                                        Conservative
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73.1%;
                                                                                                                     75.5%;
73.1%;
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Pred.
                                                                                                                       Score 909.5; DB 5
Pred. No. 7.6e-88;
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No. 7.6
-GGACDPPNHHFDLSQPIYEKIALYKSGII 114
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; NAME/KEY: peptide
; LOCATION: 1..250
; OTHER INFORMATION: Ceres Seq. ID no. 3446951
US-09-935-625-2249
         Matches 166;
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                                                                                                                                                                                                                                                                                                        Sequence 2249, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES,
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
                                           Query Match
                                                                                                                                                                                                               SEQ ID NO 2249
LENGTH: 250
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GENERAL INFORMATION
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CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
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SEQ ID NO 31520
LENGTH: 236
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TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
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CURRENT FILING DATE: 2001-08-24
                                                                                                                                                           FEATURE:
                                                                                                                                                                   ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                 TYPE: PRT
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LOCATION: 1..236
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                           Local Similarity
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       Conservative
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                 75.5%; Score 909.5; DB 5 73.1%; Pred. No. 7.6e-88;
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   Mismatches
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                                     DB 5;
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                                     Length 250;
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   Indels
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RESULT 12
US-09-935-625-23149
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CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 23149
LENGTH: 250
                                                                                                                                                                                               Sequence 23149, Application US/09935625
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
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SEQ ID NO 2253
LENGTH: 250
                                                                                                                   TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA TITLE OF INVENTION: MODULATING VARIOUS RESPONSES FILE REFERENCE: 2750-1481P
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TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
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Local Similarity 73.1%; Pred. NO. 7.6e-88;
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; OTHER INFORMATION: Ceres Seq. ID no. 3446956 US-09-935-625-2254
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                                      US-09-935-625-23154
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LENGTH: 236
Sequence 23154, Application US/09935625 GENERAL INFORMATION:
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TITLE OF INVENTION: POLYNICLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPABLE
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/935,625
CURRENT FILING DATE: 2001-08-24
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NAME/KEY: peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: peptide LOCATION: 1..236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OTHER INFORMATION: Ceres Seq. ID no. 3446952
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                                                                                                                                                                                                                115 PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
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                                                                                                                                                      175 NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
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                                                                                                                                                                                                                                                                    71 QNDGKWCLPG-SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV 129
                                                                                                                                                                                                                                                                                                      63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                                                            Match 75.5%; Score 909.5; DB 5; Length 236; Local Similarity 73.1%; Pred. No. 7.1e-88;
                                                                                                                                                                                                                                                                                                                                                                                  3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALEDQGLSCGACXELMC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
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                                                                                                                NWQSNSYLNGQSLSFKVTTSDGQTIVSNNVANAGWSFGQTFTGAQLR 236
                                                                                                                                                                                          PVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQ 189
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73.1%;
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OTHER INFORMATION: Ceres Seq. ID no. 3446956 US-09-935-625-23154
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CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
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SEQ ID NO 31516
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TITLE OF INVENTION: POLYNUCLEOTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA
TITLE OF INVENTION: MODULATING VARIOUS RESPONSES
FILE REFERENCE: 2750-1481P
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TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
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                 115 PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
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                                                       71 QNDGKWCLPG-SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV 129
                                                                                            63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 111
                                                                                                                                                    3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDOGLSCGACXELMC 62
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236
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                                                                                                                                                                                                                             75.5%; score 909.5; 73.1%; Pred. No. 7.1
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Pred. No. 7.1e-88;
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9; Mismatches 33;
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; TYPE: PRT
; ORGANISM: Glycine max
US-10-219-999-42752
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                                                                                                                                                                               APPLICANT: Stein, JOSHUS
TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: US 60/312,544
PRIOR FILING DATE: 2001-08-15
SEQ ID NO 42752
LENGTH: 264
TWEEL-THE SEA
                                                   Matches 167;
                                                                                       Query Match
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LENGTH: 205
TYPE: PRT
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TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT
FILE REFERENCE: 38-10(52726)C
CURRENT APPLICATION NUMBER: US/10/219,999
CURRENT FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: US 60/324,109
PRIOR FILING DATE: 2001-09-21
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APPLICANT: Edgerton, M
APPLICANT: Hinkle, Gre
APPLICANT: Kovalic, Da
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PRIOR FILING DATE: 2001-08-15
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3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC 62
                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               60 VTATNECEPGGWCDPPNHHEDLSQPVFQQTAQYRAGIVPVVYRRVRCMRRGGIRETINGH 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   77 VTATNFCPPGGACDPPNHHEDLSQPIYEKIALYKSGIIPVMYRRVRCKRSGGIRFTINGH 136
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RSVLSYNAAPPSWSFGQTYTGRQFRY 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNSYLNGQSLSFVVTTSDR 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  167;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          h 79.1%; Score 952.5; DB 6
Similarity 81.1%; Pred No. 1.7e-92;
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Kovalic, David K.
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Hinkle, Gregory J.
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Liu, Jingdong
                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                        75.9%; Score 913.5; DB 6; Length 264; 73.6%; Pred. No. 3.1e-88; ative 19; Mismatches 32; Indels 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 205;
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RESULT 5
US-09-935-625-2254
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CURRENT FILING DATE: 2001-08-24
NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 2250
LENGTH: 236
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-09-935-625-2250

Sequence 2250, Application US/09935625

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: POLYMUCLECTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA

TITLE OF INVENTION: MODULATING VARIOUS RESPONSES

TITLE REFERENCE: 2750-1481P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-09-935-625-2250
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                        NUMBER OF SEQ ID NOS: 33136
SEQ ID NO 2254
LENGTH: 236
TYPE: PRT
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                                                                                                                                                                                                                                                         Sequence 2254, Application US/09935625 GENERAL INFORMATION:
                                                                                                 APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: POLYNUCLECTIDES, POLYPEPTIDES, CELLS, AND METHODS THEREOF CAPA

TITLE OF INVENTION: MODULATING VARIOUS RESPONSES

FILE REFERENCE: 2750-1481P

CURRENT APPLICATION NUMBER: US/09/935,625

CURRENT FILING DATE: 2001-08-24
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Arabidopsis thaliana
FEATURE:
NAME/KEY: peptide
LOCATION: 1..236
OTHER INFORMATION: Ceres Seq. ID no. 3446952
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              130 PVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          115 PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                 175 NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                                                                                                                                         190 NWQSNSYLNGQSLSFKVTTSDGQTIVSNNVANAGWSFGQTFTGAQLR 236
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                158 PVSYRRVACRRKGGIRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWMPMSRNWGQ 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        115 PVMYRRVRCKRSGGIRETINGHSYENLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ ]74
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKTALYKSGII 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11 GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC 70
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75.5%; Score 909.5; DB 5; Length 236; 73.1%; Pred. No. 7.1e-88; Vative 19; Mismatches 33; Indels 9
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Sequence:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Post-processing: Minimum Match 0%
Maximum Match 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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Gapop 10.0 , Gapext 0.5
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Match
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// cgn2_6/ptodata/1/paa/PcT_NEW_COMB.pep:*

// cgn2_6/ptodata/1/paa/Us06_NEW_COMB.pep:*

// cgn2_6/ptodata/1/paa/Us08_NEW_COMB.pep:*

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    Listing first 45 summaries
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    DВ
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US-09-935-625-2249
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US-09-935-625-23149
US-09-935-625-31515
US-09-935-625-31515
US-09-935-625-31512
US-09-935-625-23146
US-09-935-625-23146
US-09-935-625-23145
US-09-935-625-23145
US-09-935-625-31512
US-09-935-625-31511
US-10-219-999-36624
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US-09-935-625-31511
US-10-559-4407
US-09-935-625-41355
                                                                                                                                                                                                                                                                                                                                                                                                       US-10-219-999-35819
US-10-219-999-59261
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    Sequence 35819, A
Sequence 59261, A
Sequence 2250, Ap
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Sequence 23154, A
Sequence 23154, A
Sequence 31516, A
Sequence 31516, A
Sequence 31520, Ap
Sequence 2249, Ap
Sequence 23149, Ap
Sequence 23149, A
Sequence 31515, A
Sequence 31515, A
Sequence 31516, A
Sequence 31516, A
Sequence 31517, A
Sequence 31517, A
Sequence 31511, A
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Sequence 3407, Appli
Sequence 407, Appl
Sequence 407, Appl
Sequence 41355, A
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RESULT 2 US-10-219-999-59261 ; Sequence 59261, Application US/10219999

Search completed: October 11, 2002, 15:00:59 Job time: 11.141 secs

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pollen allergen homolog, hypothetical (clone PPA1) - garden pea C;Species: Pisum sativum (garden pea) C:Date: 08-Jul-1995 #sequence_revision 21-Jul-1995 #text_change C;Accession: S65056; S53082 R;Michael, A.J.
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S53082
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C; Superfamily:
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A; Residues: 1-257 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable expansin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: D84820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Cross-references: GB: AE002093; NID: g2795809; PIDN: AAB97125.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A; Reference number: A84420; MUID:20083487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTK-WQLMSRNWG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NDDPRWCL-GSTITVTATNFCPPNPGLSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGIV 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GGWQGGHATFYGGEDASGTMGGACGYGNLYGQGYGTNTAALSTALFNNGLTCGACYEMKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   150;
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65.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 832.5; DB 2
Pred. No. 2.1e-70;
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                                        21-Jul-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Map position: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Experimental source: C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the Protein Sequence A; Reference number: 224472 A; Accession: T4/589 A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expansin-like protein - Arabidopsis thaliana
N;Alternate names: protein T22E16.160
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
C;Accession: T47689
R;Benes, V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Cross-references: EMBL: AL132975
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-260 <BEN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 B
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A;Title: A cDNA from pea petals with sequence similarity to pollen allergen,
A;Reference number: S65056; MUID:96197414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-258 <MI2>
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                                                                                  152 VPISYRRVACRKSGGIRFTINGHRYFNLVLITNVAGAGDIARTSVKGSKTGWMSLTRNWG
                                       174 QNWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                114
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                                                                                                                                                                                                              63 VNDPQWCIKGR-SIVVTATNFCPP-----GGACDPPNHHFDLSQPIYEKIALYKSGI 113
                                                                                                                                                                                                                                                        32 GSWQTAHATFYGGNDASGTMGGACGYGNLYSQGYGTNTAALSTSLFNSGQSCGACFEIKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30 GPWTSAHATFYGGSDASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGLSCGACFELKC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        V.; Wurmbach, E.; Drzonek, H.; Ansorge, W.; d to the Protein Sequence Database, February
QNWQSNAVLVGQSLSFRVTSSDRRTSTSWNIAPSNWQFGQTFVGKNFR
                                                                                                            IPVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWG
                                                                                                                                                                      VNDPKWCHPGNPSVFVTATNFCPPNLAQPSDNGGWCNPPRSHFDLAMPVFLKIAEYRAGI
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                                                                                                                                                                                                                                                                                                                                                                   68.6%;
64.5%;
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                                                                                                                                                                                                                                                                                                                                               27; Mismatches
                                                                                                                                                                                                                                                                                                                                                              Score 825.5; DB 2
Pred. No. 9.5e-70;
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R:Lln, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: cultivar Columbia
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A;Cross-references: EMBL:AC004684; NID:g3236234; PID:g3236246
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C; Superfamily: expansin
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A; Accession: C84795
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A; Residues: 1-262 <STO>
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A; Introns: 54/1; 160/2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expansin - upland cotton
C;Species: Gossypium hirsutum (upland cotton)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C;Accession: T09786
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A;Title: Specific expression of an expansin gene during elongation of cotton fibres.
A;Reference number: Z14468; MUID:9655931
A;Accession: T09786
                                                                                                                                                                                                                              C;Function:
A;Description: involved in cell wall modification
C;Superfamily: expansin
                                                                                                                                                                                                                                                                                                               A; Experimental source: cultivar Siokra \tilde{\mathbf{1}}-2 C; Genetics:
                                                                                                                                                                                                                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-258 <ORF>
A; Cross-references: EMBL: AF043284; NID: 92811277; PID: 92811278
                                                                                                                                                                                                                                                                                               A; Gene: GhEX1
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                    63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSOPIYEKIALYKSGII 114
                                                            34 GGWQTAHATFYGGADATGTMGGACGYGNLYSQGYGTSTAALSTALFNNGLSCGACYELRC 93
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                                                                                                                                                                        70.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25;
                                                                                                                                                        25; Mismatches
                                                                                                                                                                          Score 852.5; DB . Pred. No. 2.8e-72
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      DB 2;
                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        40; Indels
                                                                                                                                                               39;
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                                                                                                                                                                                                   Length 258;
                                                                                                                                                               Indels
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expansin-like protein TIE22.20 [similarity] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           δõ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Reference number: Z24489
A; Accession: T48247
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the Protein Sequence Database, March 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-258 <BEV>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; Bevan, M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Note: TIE22.20
C; Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Experimental source: cultivar Columbia; BAC clone T1E22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Cross-references: EMBL: AL162874
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        밁
                                                                                                                                                                                                                                   R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Unayam, L.; Tailon, euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
                                                                                                                                                                                                                                                                                                                       probable expansin (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
                                                                                                                                              C; Accession: F84831
                                                          A;Cross-references: GB:AE002093; NID:g2651297; PIDN:AAB87577.1; GSPDB:GN00139
                                                                                    A; Molecule type: DNA
A; Residues: 1-253 <S
                  A; Gene: At2g40610
                                            C;Genetics:
                                                                                                                            A; Status: preliminary
A; Map position:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          174 ONWOSNSYLNGOSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      114 IPVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210 ONWOSNALLVGOSLSFRVKTSDGRSSTSNNIAPSNWQFGQTYSGKNFR 257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 INDPGWCLPGNPSILITATNECPPNENQASDNGGWCNPPREHEDLAMPMELSTAKYKAGI 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 VNDPQWCIKGR-SIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGI 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30 GPWINAHATTYGEADASGTMGGACGYGNLYSQGYGVNTAALSTALFNNGLSCGSCFELKC 89
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T48247
                                                                                         1-253 <STO>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70.2%; Score 845.5; DB 2; 67.5%; Pred. No. 1.3e-71; ative 22; Mismatches 43;
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A;Experimental source: cultivar Burpee Pickler C:Genetics:
A;Gene: Expl
C:Function:
A;Description: mediates cell wall extension
C:Superfamily: expansin
C:Superfamily: expansin #status predicted
F;24-250/Product: expansin #status predicted <MAT
                                                                                                                                                                                                                                                                                                                                                                                     C;Species: Cucumis sativus (cucumper)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10079
C;Accession: T0079
                                                                                                                                                                                         A;Cross-references: EMBL:U30382; NID:91040874; PIDN:AAB37746.1; PID:91040875
                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-250 <SHC>
                                                                                                                                                                                                                                                                                          A:Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi
A:Reference number: Z14894; MUID:96016146
A:Accession: T10079
                                                                                                                                                                                                                                                                        A:Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                       R;Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Shieh Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                expansin S1 precursor - cucumber
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:U64890; NID:91778098; PID:91778099
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A;Reference number: Z16866
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C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Accession: T09818 R; Hutchison, K.W.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library, July 1996
A;Description: Expansing are conserved in conifers and expressed in response to exoge
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T09825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: clone pPtexp4
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A; Residues: 1-232 <HUT>
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A; Accession: T09825
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                                                                                                          175 NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQ 219
                                                                    187 NWQSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSNWQFGQTFEGSQ 231
                                                                                                                                                  127 PILYTRVPCLRKGGIRFTVNGHSCFNLVLITNVGGAGDVHAVSIKGPRSGWQPMSRNWGQ 186
                                                                                                                                                                                                                                68 NDDPQWCLPG-TVTITATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIV 126
                                                                                                                                                                                                                                                                           63 VNDPQWCIKGRSIVVTATNFCPP-----GGACDPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          205 NWQSNNYLNGQGLSFQVTLSDGRTLTAYNLVPSNWQFGQTYEGPQF 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  175 NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      145 PVSFRRVPCMKKGGVRFTINGHSYFNLVLITNVGGAGDVHSVSIKGSRTGWQSMSRNWGQ 204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                115 PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                                                                                                                                                                                                                                                           3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63 VNDPQWCIKGRSIVYTATNFCPP-----GGACDPPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           26 GGWQSGHATFYGGGDASGTMGGACGYGNLYSQGYGTNTVALSTALFNNGLSCGACFEMTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC 62
                                                                                                                                                                             PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                                                                                                                                                                                                                   GGWESAHATTFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMQC 67
                                                                                                                                                                                                                                                                                                                                                                                                                    154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        152; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  71.1%; Score 856.5; 68.4%; Pred. No. 1e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   71.2%; Score 857.5; DB 2; Length 250; 67.3%; Pred. No. 9.2e-73;
                                                                                                                                                                                                                                                                                                                                                                                                         24; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26; Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                Pred.
                                                                                                                                                                                                                                                                                                                                                                                                                             No. 1e-72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                            38;
                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 232;
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                                                                                                                                                                                                                                                                                                                                                                                                       9
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A;Description: Arabidopsis thaliana chromosome II BAC F13M22 genomic sequence. A;Reference number: Z14677 A;Reference number: T02530 A;Status: translated from GB/EMBL/DDBJ

A; Molecule type:

C; Accession: T02530; C84795 R; Rounsley, S.D.; Kaul, S.;

submitted to the EMBL Data Library,

S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; ata Library, June 1998

probable expansin r13M22.14 - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 05-Mar-1999 #sequence\_revision 05-Mar-1999 #text\_change 16-Feb-2001

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C; Genetics:
A; Gene: EXP1
C; Function:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Molecular cloning and sequence analysis of expansins -- a highly conserved, multi
A;Reference number: Z14894; MUID:96016146
A;Accession: T50654
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Description: induces extension (creep) in plant cell walls C;Superfamily: expansin C;Keywords: cell wall
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Molecule type: mRNA
A;Residues: 1-237 <SHC>
A;Cross-references: EMBL:U30476; PIDN:AAB38070.1
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C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C:Accession: C84444
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487 A;Accession: C84444
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Elsen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, C. Nature 402, 761-768, 1999
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₽В
                                                                                                                                                                                                                                                                                                                                                                                                            A; Map position: 2
C; Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: GB:AE002093; NID:g3461833; PIDN:AAC32927.1; GSPDB:GN00139 C;Genetics:
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A; Residues: 1-248 <STO>
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                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                  Matches 163; Conservative
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                           144 SYRRVPCMRRGGIRFTINGHSYFNLVLVTNVGGAGDVHSVAVKGSRTRWQQMSRNWGQNW 203
                                                                      117 MYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNW 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12
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                                                                                                                                                                                                                                                                                                                                        Local Similarity
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                                                                                                                                                                   65 DPQWCIKGRSIVVTATNECPP------GGACDPPNHHEDLSQPIYEKIALYKSGIIPV 116
                                                                                                                                                                                                                25 WVNAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIKCQS 84
                                                                                                                                                                                                                                                               5 WINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMCVN 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GGWYNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQ 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QNDGKWCLPG-SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWQSNSYLNGQSLSFKVTTSDGQTIVSNNVANAGWSFGQTFTGAQLR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                        DGAWCLPG-AIIVTATNFCPPNNALPNNAGGWCNPPLHHFDLSQPVFQRIAQYKAGVVPV 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          75.5%;
                                                                                                                                                                                                                                                                                                             75.4%; Score 907.5; DB 2; 72.4%; Pred. No. 1.9e-77; tive 24; Mismatches 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19; Mismatches
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                                                                                                                                                                                                                                                                                                                       Indels
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C;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C;Accession: T09821
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A; Accession: T09821
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expansin (clone pPtexp5) - loblolly pine (fragment)
C;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C;Accession: T09826
R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Molecule type: mRNA
A; Residues: 1-232 <HUT>
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                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Reference number: Z16866
A; Accession: T09826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library, July 1996
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A; Residues: 1-232 <HUT>
                 g
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                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   175 NWQSNSYLNGQSLSEVVTTSDRRSVVSENVAPPTWSFGQTYTGGQ 219
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 114
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                    68
                                                            63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSG11 114
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                                                                                                                                       GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALEDQGLSCGACXELMC 62
                                                                                                         GGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMQC 67
                 NDDPQWCLPG-TVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIV 126
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                                                                                                                                                                                                                                 Score 864.5; DB 2
Pred. No. 1.9e-73;
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\begin{array}{c} 799 \\ 399 \\ 375 \\ 375 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\ 377 \\
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Copyright (c) 1993 - 2002 Compugen Ltd.
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| Qy 181 YLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTRYTGGQFRY | Qy 121 VRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNS<br> | Qy 61 MCVNDPQWCIKGRSIVVTATNECPPGGACDPPNHHEDLSQPIYEKIALYKSGIIPVMYRR | Qy 1 HMGPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXEL | Query Match 99.3%; Score 1195; Best Local Similarity 97.7%; Pred. No. 2.5 Matches 217; Conservative 0; Mismatches | A;Description: induces extension (creep) in plant C;Superfamily: expansin C;Keywords: cell wall | A;Cross-references: EMBL:U30478; PIDN:AAB38071 A;Experimental source: variety Columbia C;Genetics: A;Gene: EXP5 C:Function: | A:Status: preliminary; translated from GB/EMBL/DDBJ<br>A:Molecule type: mRNA<br>A:Residnes: 1-255 < GROCY | .M.<br>924:<br>ana<br>46                                                                            | RESULT T50655 T50675 T50675 Expansin EXP5 [imported] - Arabidopsis thaliana c. Species: Arabidopsis thaliana (mouse-ear cresc.) pate: 21-Jul-2000 #sequence_revision 21-Jul-2C; Accession: T50655 | ALIGNMENTS | 36 278.5 23.1 259 2 T50557<br>37 278.5 23.1 271 2 H84592<br>38 257.5 21.4 276 2 T09041<br>39 256 21.3 102 2 T09828<br>40 252.5 21.0 277 2 S48032<br>41 250 20.8 77 2 T09815<br>42 241 20.0 491 2 F96681<br>43 237 19.7 261 2 T04301<br>44 225.5 18.7 263 2 S13614<br>45 224 18.6 259 2 E84886                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 725 60.2 261 2<br>698 58.0 255 2<br>624.5 51.9 257 2<br>620.5 51.5 257 2<br>598.5 49.2 160 2<br>548.6 256 256 |
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| QFRY 222                                           | KGSRTKWQLMSRNWGQNWQSNS 180                                              | SQPIYEKIALYKSGIIPVMYRR 120<br>                                     | ETAALSTALFDQGLSCGACXEL 60                                         | DB 2; Length 255;<br>ie-104;<br>s 5; Indels 0; Gaps 0;                                                            | nt cell walls                                                                                   |                                                                                                                             | DADC                                                                                                      | ; Guiltinan, M.J.; McQueen-Mason, S.J.; Shi<br>9, 1995<br>alysis of expansinsa highly conserved, mu | 1<br>18)<br>1000 #text_change 28-Jul-2000                                                                                                                                                         |            | beta-expansin [imp beta-expansin [imp beta-expansin [imp ciml protein home] expansin (clone pp ciml protein flore pD protein flore pD protein flore pD protein flore pD protein flore flore pD protein flore flore pD protein flore flore pD protein flore flore pD protein flore flore flore pD protein flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flore flo | expansin - rice expansin 3 - rice expansin 3 - rice hypothetical prote protein T12C24.10 expansin - upland    |

expansin EXP1 [imported] - Arabidopsis thaliana (fragment) (Species: Arabidopsis thaliana (mouse-ear cress) (C;Species: Arabidopsis thaliana (mouse-ear cress) (C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 02-Sep-2000 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Accession: T50654 (Acce

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        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                               N11m1 A., Harata M., Mizuno S.;
"Chicken DNA topoisomerase 2 alpha and beta.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: CONTROL OF TOPOICGICAL STATES OF DNA BY TRANSIENT
BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. TOPOISOMERASE II
MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TP2A_CHICK 042130;
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SEQUENCE
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                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The CCT 2001 (Ref. 40, Last annotation update)
DNA topoisomerase II, alpha isozyme (EC 5.99.1.3).
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID-9031;
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16-OCT-2001 (Rel.
16-OCT-2001 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               84 NLHKFKLHSYGSPTFCDHCGSLLYGLLHQGLKCDSCDMNVHKRCEKNVPLLCGTDHTERR 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                     MISCELLANDOUS: EUKARYOTIC TOPOISOMERASE I AND II CAN RELAX BOTH NEGATIVE AND POSITIVE SUPERCOILS, WHEREAS PROKARYOTIC ENZYMES RELAX ONLY NEGATIVE SUPERCOILS.

SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                    of double-stranded DNA.
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                CATALYTIC ACTIVITY: ATP-dependent breakage, passage and rejoining
                                                                                                                                                                                                   SUBCELLULAR LOCATION: NUCLEAR; GENERALLY LOCATED IN THE
                                                                                                                                                                                        NUCLEOPLASM.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRN 171
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -----QWCIKGRSIVV---TATNFCP--PGGACDPPNHHFDLSQPIYEKIALYKSGIIPV 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E; PS50004; C2_DOMAIN_2; 1.
E; PS00479; DAG_PE_BIND_DOM_1; 2.
E; PS50081; DAG_PE_BIND_DOM_2; 2.
E; PS500107; PROTEIN_KINASE_ATP; 1.
E; PS50011; PROTEIN_KINASE_DOM; 1.
E; PS00108; PROTEIN_KINASE_ST; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
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40, Last sequence update)
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ATP (BY SIMILA
BY SIMILARITY.
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Pred. No. 6
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6.9;
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ACT_SITE
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SMART; SM00433; TOP2c; 1.
SMART; SM00434; TOP4c; 1.
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PRINTS; PRO0418; TPI2FAMILY.
PRODOM: PD000616; DNA_topoisoII; 1.
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InterPro; IPR002205; DNA_topoisoIV.
InterPro; IPR003205; DNA_TopoisoIV.
InterPro; IPR003594; HATPase_c.
Pfam; PF00204; DNA_topoisoII; 1.
Pfam; PF00521; DNA_topoisoIV; 1.
                                                                                                                                                                                                                                                                                                                  SEQUENCE
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HSSP; P06786; 1
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                                                                   NSYLNGQSLSFVVTTSDRRSV 199
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                                                                                                                                                                                                       DEKKYTGGRNGYGAKLCNIFSTKFTVET------ACREYKKLFKQTWTDNM 199
                                           VSFVNS----IATTKGGRHV
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                                                                                                                        GGIRFTING-----HSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQS 178
                                                                                                                                                                          GRSIVVTATNFCPPGGAC---DPPNHHFDLSQPIYEKIALYKSGIIPVMYRRVR--CKRS 126
                                                                                                                                                                                                                               DAXXTMGGACGYG----NLYSQGYGLETAALSTALFDQGLSCGACXELMCVNDPQWCIK- 71
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e; Topoisomerase; DNA-binding; ATP-binding; Nuclear protein.
162 167 ATP (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                 В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 14
                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Characterization of a cDNA encoding a cytosolic peptidylprolyl cistrans-isomerase from Blattella germanica.";
Eur. J. Biochem. 234:284-292(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta
Pterygota; Neoptera; Orthopteroidea; Dictyoptera; Blattaria;
Blaberoidea; Blattellidae; Blattellinae; Blattella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-0CT-1996 (Rel. 34, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Peptidyl-prolyl cis-trans isomerase (EC 5.2.1.8)
(Cyclophilin) (Cyclosporin A-binding protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam; PF00160; pro_isomerase; PRINTS; PR00153; CSAPPISMRASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
Aplysia californica (California sea hare)
                   PRKC1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cyclosporin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00170; CSA_PPIASE_1; 1.
PROSITE; PS50072; CSA_PPIASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HSSP; P05092;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; X87418; CAA60869.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=6973;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Blattella germanica (German
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISSP; P05094; 2012.
InterPro; IPR002130; CSA_PPIase.
                                                                                                                                                                                                             123
                                                                                                                                                                                                                                              195
                                                                                                                                                                                                                                                                                                                 144
                                                                                                                                                                                                                                                                                63
                                                                                                                                                                                                                                                                                                                                                                                   92
                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                   4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ENZYME REGULATION: BINDS CYCLOSPORIN A (CSA). CSA MEDIATES OF ITS EFFECTS VIA AN IMHIBITORY ACTION ON PPIASE. SUBCELLULAR LOCATION: CYTCOPLASMIC.
TISSUE SPECIFICITY: UBIQUITOUS.
SIMILARITY: BELONGS TO THE CYCLOPHILIN-TYPE PPIASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   European
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC ACTIVITY: Peptidylproline (omega=180) =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FUNCTION: PPIases accelerate the folding of proteins the cis-trans isomerization of proline imidic peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             oligopeptides
                                                                                                                                                                                                                                                                                                               ----VTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNSYLNGQSLSFVVTTS----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                             DNRHVV--
                                                                                                                                                                                                                                              DRRSVVSFNVAPPTWSFGQTYTG
                                                                                                                                                                                                                                                                              QGGDFTNHNGTGGKSIYGTKFEDENFQLKHTGPGILWMANAGPNTNGSQFFITTAKTSWL 122
                                                                                                                                                                                                                                                                                                                                                                                 PNHHFDLS---QPIYEKIALYKSGIIPVMYRRVRCKRSGGIRFTINGHSYFNLVL----
                                                                                                                                                                                                                                                                                                                                                     PRVFFDMSADGQPVGRIVMELRSDVVPKTAENFRÄLCTGEKGFGYKG-SRFHRVIPNFMC
                                                                                                                                                                                                                                                                                                                                                                                                                    36; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        164 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Isomerase;
                                                                                                                       STANDARD;
                                                39, Created)
39, Last sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence of the sequence
                                  protein kinase
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25.2%;
                                                                                                                                                                                                             -FGSVVEG
                                Last sequence update)
Last annotation updat
tein kinase C (EC 2.7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Rotamase
                                                                                                                                                                                                                                                                                                                                                                                                                      14;
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                                                                                                                                                                                                             135
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 79;
                                                                                                                                                                                                                                              217
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred.
                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A5E25B574DFCDC99 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                        No.
                                  10n update)
(EC 2.7.1.
                                                                                                                        649
                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 1;
                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                      65;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 164;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (PPIase) (Rotamase)
                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIATES SOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptidylproline
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             It catalyzes bonds in
                                                                                                                                                                                                                                                                                                                                                                                                                       28;
                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                     143
                                                                                                                                                                                                                                                                                                                  194
                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                                                                                                                                                                                                                                                                                                                      5
   between
                                                  SMART;
                                                                                   Pfam; PF00433; pkinase_C; 1.
PRINTS; PR00360; C2DOMAIN.
PRINTS; PR00008; DAGPEDOMAIN
                                                                                                                                                                                                                                                                                  HSSP;
                                                                                                                                                                                                                                                                                                                                                                                       use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -
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                                                                                                                                                           Pfam;
                                                                                                                                                                                                                                                                                                                                                     entities
                                                                                                                                                                                                                                                                                                                                                                   modified
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ERRATUM
   PROSITE;
                                                                                                                                                                             Pfam;
                                                                                                                                                                                           InterPro; IPR000961; InterPro; IPR002290;
                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEMBRANES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SIMILARITY)
                                                                                                                                          PF00069;
                                                                                                                                                         PF00168; C2; 1.
PF00130; DAG_PE-bind;
                                                                                                                                                                                                                                                                                  P05697;
                                                      SM00109; C1; 2
SM00239; C2; 1
                     SM00220;
   PS00499;
                   S_TK_X; 1.
S_TKC; 1.
                                                                                                                                          pkinase; 1.
```

C2\_DOMAIN\_1;

Ser\_thr\_pkinase

N

Pkinase\_C

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"Characterization of two isoforms of protein system of Aplysia californica.";
J. Biol. Chem 260.5777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pepio A.M., Fan X., Sossin W.S.;
J. Biol. Chem. 273:22856-22856(998).
-i- FUNCTION: THIS IS CALCIUM-DEPENDENT, PHOSPHOLIPID-DEPENDENT,
SERINE- AND THREONINE-SPECIFIC ENZYME. ACTIVATION OF PKC BY
SEROTONIN RESULTS IN PRESYNAPTIC FACILITATION OF DEPRESSED
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=91332620; PubMed=1869917;
Kruger K.E., Sossin W.S., Sacktor
                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the El
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHARACTERIZATION.
MEDLINE=98334636; PubMed=9668085;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93194877; PubMed=8449941;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Aplysiidae; Aplysia.
NCBI_TaxID=6500;
                                                                                                                                or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              J. Biol. Chem. 273:19040-19048(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pepio A.M., Fan X., Sossin W.S.;
"The role of C2 domains in Ca2+-activated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  independent PKCs expressed in Ap
J. Neurosci. 11:2303-2313(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Cloning and characterization of
                                            InterPro; IPR000008;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CHARACTERIZATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Mollusca;
                                                                                                                                                                        een the Swiss Institute. Tr
European Bioinformatics Institute. Tr
non-profit institutions as long
                                                                                                                                                                                                                                                                                                                          SIMILARITY: CONTAINS 1 SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                                     BINDING DOMAINS
                                                                                                                                                                                                                                                                                                                                                                                                                                      SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          ENZYME REGULATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     THE RECEPTOR FOR PHORBOL ESTERS, A CLASS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FUNCTION: PKC IS ACTIVATED BY DIACYLGLYCEROL WHICH IN TURN PHOSPHORYLATES A RANGE OF CELLULAR PROTEINS. PKC ALSO SERVI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SENSORY-TO-MOTOR NEURON SYNAPSES, WHICH IS THOUGHT BEHAVIORAL DISHABITUATION.
                                                                                       M94883; AAA27770.1;
                                                                                                                                                                                                                                                                                                        SUBFAMILY
                                                                                                                                                  non-profit institutions as long as its content
and this statement is not removed. Usage by an
requires a license agreement (See http://www.isb
  IPR002219;
IPR000719;
                                                                     1TBN
                                                                                                                                                                                                                                                                                                                                                                                           CONTAINS 2
Euk_pkinase.
                          DAG_PE-bind
                                                                                                                                                                                                                                                                                                                                                                                                                                    ACTIVATED BY PH
ON: CYTOPLASMIC;
                                                                                         ALT_TERM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sacktor T.C.,
                                                                                                                                                                                                                                                                                                                            THE
                                                                                                                                                                                                                                                                                                                                                   C2 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                           ZINC-DEPENDENT PHORBOL-ESTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of Ca(2+)-dependent and Aplysia sensory cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gastropoda; Opisthobranchia; Anaspidea;
                                                                                                                                                                                                                                                                                                                            SER/THR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                    PHOSPHATIDYLSERINE IC; TRANSLOCATED TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           protein kinase
                                                                                                                                                                                                                     There are no
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Ca2+-independent protein
                                                                                                                                                    . Usage by and for commercial http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OF.
                                                                                                                                                                                                                                                                                                                               OF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TUMOR PROMOTERS
                                                                                                                                                                                                                                                                                                                               PROTEIN KINASES
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                                                                                                                                                                                                                       restrictions
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                                                                                                                                                                                                                                              outstation
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RESULT 12
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Best Local !
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InterPro: IPR000169; ThiolprotLact
Pfam; PF00112; Peptidase_C1; 1.
PRINTS; PR00705; PAPAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS00139; THIOL_PROTEASE_CYS; 1.

PROSITE; PS00639; THIOL_PROTEASE_HIS; 1.

PROSITE; PS00640; THIOL_PROTEASE_ASN; 1.

Hydrolase; Thiol protease; Lysosome; Glycoprotein; Zymogen; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PDB; 2PBH; 25-FEB-98.
PDB; 3PBH; 25-FEB-98.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SWISS-2DPAGE; P07858; HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MIM; 116810;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEROPS; C01.060;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ACT_SITE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DISULFID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VARIANT

¶Oka C., Soma A., Kanda H.,

                                                                                                                                                                                             MOUSE
                                                                                                   HRAL_MOUSE STANDARD; PRT; 480 AA. 09R118; 09R118; 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update) Serine protease HTRA1 precursor (EC 3.4.21.-). PRSS11 OR HTRA1 OR HTRA.
                                                                                                                                                                                                                                                                                                                                                                                                  126 NAHVSVEVSAEDLLTCCGSMCGDG--CNGGYPAEAWNEWTRKGLVSGGLYESHVGCRPYS 183
                                                             Eukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                      103 YEK-----IALYKSGIIPVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGA 150
                                                                                                                                                                                                                                                                                                                                                 184 IPPCEHHVNGSRPPCTGEGDTPKCSKICEPGYSPTYKQDKHYGYNSYSVSNSEKDIMAEI 243
           STRAIN-ICR;
                           SEQUENCE FROM N.A.
                                              NCBI_TaxID=10090;
                                                                                      Mus musculus (Mouse)
                                                                                                                                                                                                                                                                    151 GDVHSVSMKG----SRTKWQLMSRNWGQNWQSNSY---LNGQ 185
                                                                                                                                                                                                                                              278 ---HAIRILGWGVENGTPYWLVANSWNTDWGDNGFFKILRGQ 316
                                                                                                                                                                                                                                                                                               244 YKNGPVEGAFSVYSDFLLYKSGV----YQHVTGEMMGG-----
                                                                                                                                                                                                                                                                                                                                                                                                                           7 NAHATF-YXXGDAXXTMGGACGYGNLYSQGYGLET-----AALSTALFDQGLSCGACX 58
                                                                                                                                                                                                                                                                                                                                                                         ELMC---VNDPQWCIKGRSIVVTATNFCPPG-------GACDPPNHHFDLSQPI 102
                                                                                                                                                                                                                                                                                                                                                                                                                                                      44; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         339 AA;
                TISSUE-Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           228
37807 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7.0%; Score 84; DB 1; Length 339; 19.8%; Pred. No. 0.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thiolprot_act_site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        24;
    Kawaichi M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /FTId-VAR_006724.
N -> D (IN REF. 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-LINKED (GLCNAC.
V -> L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ACTIVATION PEPTIDE.
CATHEPSIN B.
CATHEPSIN B LIGHT CHAIN.
CATHEPSIN B HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 -> D (IN REF. 4).
06D5FE184AE47070 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                            80; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            74;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                            В
                                                                                                                                                                     Qy
                                                                                         Db
                                     RESULT 13
CYPH_BLAGE
                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation between the Suropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -i- SIMILARITY: CONTAINS 1 IGFBP DOMAIN.
-i- SIMILARITY: CONTAINS 1 KAZAL-LIKE DOMAIN.
-i- SIMILARITY: CONTAINS 1 PDZ/DHR DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00219; IGFBP; 1.
Pfam; PF00050; kazal; 1.
Pfam; PF00595; PDZ; 1.
Pfam; PF00089; trypsin; 1.
PFINTS; PR00834; PROTEASES2C.
                                                                                                                                                                                                                                                                                                                                                         ACT_SITE
ACT_SITE
ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMART; SM00121; IB; 1.
SMART; SM00280; KAZAL; 1.
SMART; SM00228; PDZ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MGD; MGI:1929076; Prss11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF172994; AAD49422.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hydrolase; Serine protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000867; IGFBP.
                                                                                                                                                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS50106;
                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
P54985;
01-OCT-1996 (Rel. 34, Created)
                           CYPH_BLAGE
                                                                                        228 VKVELK------NGATYEAIIKDVDEKADIA 252
                                                                                                                 163 TKWQLMSRNWGQNWQSNSYLNGQSLSFVVTTSDRRSVVS 201
                                                                                                                                           183 VVKHELYRK--LPFSKREVPVASGSGFIVSEDG-----LIVTN-----AHVVTNK-NR
                                                                                                                                                                                              125 --TYTNLCQLRAASRRSEKLPQPPVIVLQRGACGQGQEDPNSLRHKYNFIADVVEKFAPD 182
                                                                                                                                                                                                                                                                                                                   Match 6.7%; Score 81; Local Similarity 21.9%; Pred. No.
                                                                                                                                                                                                                         76 VVTATNEC------PP-----GGAC----DPPN---HHEDLSQPIYEKIA-- 107
                                                                                                                                                                                                                                                    73
                                                                                                                                                                                                                                                                             16 GDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMCVNDPQWCIKGRSI 75
                                                                                                                                                                                                                                                   GAACGLQEGPCGEGLQCVLPFGVPASATVRRRAQAGLCVCASSEPVCGSDAK------ 124
                                                                                                                                                                     -----LYKSGIIPVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSR 162
                                                                                                                                                                                                                                                                                                           48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IPR001254; Trypsin. IPR002350; kazal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IPR001478; PDZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR001940; Protease2C.
                                                                                                                                                                                                                                                                                                                                                              480 AA;
                                                                                                                                                                                                                                                                                                           Conservative
                           STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PDZ; 1
                                                                                                                                                                                                                                                                                                                                                                                       480
94
155
364
467
220
250
                                                                                                                                                                                                                                                                                                                                                               51246 MW;
                                                                                                                                                                                                                                                                                                            26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Growth factor binding; Signal.
                                                                                                                                                                                                                                                                                                                                                                           CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
CHARGE RELAY SYSTEM (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SERINE PROTEASE HTRA1
                                                                                                                                                                                                                                                                                                                                                                                                                                 SERINE PROTEASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                             KAZAL-LIKE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                               54BB9BA6C99A7BF4 CRC64;
                                                                                                                                                                                                                                                                                                             Mismatches
                               164 AA
                                                                                                                                                                                                                                                                                                                                       DB 1; Length 480;
                                                                                                                                                                                                                                                                                                               73; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          (POTENTIAL).
                                                                                                                                                                                                                                                                                                                  72;
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RESULT 11
CATB_HUMAN
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           Cao L., Taggart R.T., Berquin I.M., Moin K., Fong D., Sloane B.F. "Human gastric adenocarcinoma cathepsin B: isolation and sequenci of full-length cDNAs and polymorphisms of the gene.";
                                                                                                                                                                                                                                                                      01-AUG-1988
01-JUL-1989
16-OCT-2001
         Gene 139:163-169(1994)
                                                                                                                                        MEDLINE=87017021; PubMed=3463996; Chan S.J., San Segundo B., McCormick M.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Outer membrane; SIGNAL 1
CHAIN 27
CONFLICT 14
CONFLICT 375
CONFLICT 606
                                                       MEDLINE=94156194; PubMed=8112600;
                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                               Cathepsin B p
CTSB OR CPSB.
                                                                                                                                                                                                                                                                                                           CATB_HUMAN P07858;
                                                                                                                            *Nucleotide and predicted amino acid sequences of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                     403 EYTG 406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam;
                                                                     SSUE=Gastric
                                                                                                                                                                                                                                                                                                                                                                                                                                     349
                                                                                                                                                                                                                                                                                                                                                                                                                                                              162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   114 IPVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGA-----GDVH------SVSMKGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                            214 TYTG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR003357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6 INAHATEYXXGDAXXTMGGACGYGNLYSQG------YGL--ETAALSTALFDQGLSCG 55
                                                                                                                                                                                                                                                                                                                                                                                                                            RTSLPFL--NGIHLLQNAKFLKLQARNGYSIEFYDPITSEADGSTQLNINGDPK----NK
                                                                                                                                                                                                                                                                                                                                                                                                                                                  RTKWQLMSRNWGQNWQSNSYL----NGQSLSF---VVTTSDRRSVVSFNVAPPTWSFGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VNQAETRFAQNTAKNGSGGA-----LYSDGDIDIDQNAYVLFRENEALTTAIGKGGAVC-
                                                                                                                   preprocathepsin B cDNAs."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -GAIYARKLSISSGGPTLFINNISYAN----SQNLGGAIAIDTGGEISLSAEKGTITFQGN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACXELMCVNDPQWCIKGRSIVVTATNFCPPGGACDP-PNHHF-DLSQPIYEKIALYKSGI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PF02415; DUF145; 1. PF02385; OMP; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CP0770;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AJ133035; CAB37075.1; -. AE001585; AAD18163.1; -. AE002237; AAF38570.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AP002545; BAA98215.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR003368;
                                                                                                           Acad.
                                                                                                                                                                                                                                                    (Rel. 11, Last sequence update)
(Rel. 40, Last annotation update)
precursor (EC 3.4.22.1) (Cathepsin
                                                                                                                                                                                                                                                                                             (Rel. 08, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   922 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                     carcinoma;
                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal; Multigene family; Complete proteome
                                                                                                      Sci. U.S.A. 83:7721-7725(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100457 MW;
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MO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----PTSGSSTPVPIVTFSDNKQLVFERNHSIMGG-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 84.5;
Pred. No. 2
                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           F -> L (IN REF. 1).
Y -> C (IN REF. 1).
D -> N (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROBABLE OUTER MEMBRANE PROTEIN PMP1. F -> L (IN REF. 1). Y -> C (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DFF2AB6333AB031C CRC64;
                                                                                                                                                                                                                                                                                                                      339 AA
                                                                                                                                           Steiner D.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                81;
                                                                                                                                                                                                                                                     B1) (APP secretase).
                                                                                                                              cloned
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 922;
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                          sequencing
                                                                                                                            human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             75;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     213
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15;
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PIR; PIR;

S16514; A25432; A25432. S16513; S16513. A26498; KHHUB L16510; M13230;

1HUC; 1CSB;

03-APR-96. 25-FEB-98. 26-JAN-95 ; S16513. ; S16514. PIR;

EMBL; M14221;

AAA52129.1; -. AAC37547.1; -. AAA52125.1;

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There are no restrictions

the European Bioinformatics Institute.

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J. Mol. Biol. 271:774-788(1997).

1. FUNCTION: THIOL PROTEASE WHICH IS BELLEVED TO PARTICIPATE IN INTRACELULAR DEGRADATION AND TURNOVER OF PROTEINS. HAS ALSO BEEN IMPLICATED IN TUMOR INVASION AND METASTASIS.

1. CAPALYTIC ACTIVITY: HYDROLYSES PROTEINS, WITH A SPECIFICITY RESEMBLING THAT OF PAPAIN.

2. RESEMBLING THAT OF PAPAIN.

2. SUBUNIT: DIMER OF A HEAVY CHAIN AND A LIGHT CHAIN CROSS-LINKED BY A DISULFIDE BOND.
                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Podobnik M., Kuhelj R., Turk V., Turk D.;
"Crystal structure of the wild-type human procathepsin B at 2.5-A resolution reveals the native active site of a papain-like cystein protease zymogen.";
J. Mol. Biol. 271:774-788(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=97446326; PubMed=9299326;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            X-RAY CRYSTALLOGRAPHY (3.2 ANGSTROMS).
MEDLINE=96197789; PubMed=8617355;
Turk D., Podobnik M., Kuhelj R., Dolinar M., Tu
"Crystal structures of human procathepsin B at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           resolution reveal an interaction motif between a papain-like cysteine protease and its propeptide.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Musil D., Zucic D., Turk D., Engh R.A., Mayr I., Huber R., Popovic T. Turk V., Towatari T., Katunuma N., Bode W.;
"The refined 2.15 A X-ray crystal structure of human liver cathepsin B: the structural basis for its specificity.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Moin K., Day N.A., Sameni M., Hasnain S., Hirama T., Sloane B.F.; "Human tumour cathepsin B. Comparison with normal liver cathepsin B.", Biochem. J. 285:427-434(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEBS Lett. 384:211-214(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBO J. 10:2321-2330(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91330854; PubMed=1868826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   X-RAY CRYSTALLOGRAPHY (2.15 ANGSTROMS).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=92344620; PubMed=1637335;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 80-91 AND 129-139.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 131-339 FROM N.A. MEDLINE=86206063; PubMed=3010323; Fong D., Calhoun D.H., Hsieh W.-T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cathepsin B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ritonja A., Popovic T., Turk V., Wiedenmann K., Ma
"Amino acid sequence of human liver cathepsin B.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ong D., Calhoun D.H., Hsieh W.-T., Lee E I ISOLation of a cDNA clone for the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FEBS Lett. 181:169-172(1985).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=85127484; PubMed=3972105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 80-126 AND 129-333.
                                                                                                                                                                                                                                                                                                                                           SUBCELLULAR LOCATION: Lysosomal SIMILARITY: BELONGS TO PEPTIDAS:
                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE PAPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Natl. Acad. Sci. U.S.A. 83:2909-2913(1986)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lysosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         a papain-like cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Turk V.; at 3.2- and 3.3-A
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RESULT
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Q9R014; Q9WV51;
16-OCT-2001 (Rel
16-OCT-2001 (Rel
                       DISULFID
DISULFID
DISULFID
CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRAIN-C57BL/6; TISSUE-Placenta;
Sol-Church K., Frenck J., Troeber D., Mason R.W.;
"Cloning of a mouse cysteine protease.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tisljar K., Deussing J., Peters C.; "Cathepsin J, a novel murine cysteine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia; NCBI_TaxID=10090;
              CARBOHYD
                                                                                                                                            Hydrolase;
SIGNAL
                                                                                                                                                                                                                Pfam; PF00112; Peptidase_C1;
                                                                                                                                                                                                                       MEROPS; C01.038; -...
MGD; MGI:1349426; Ctsj.
InterPro; IPR000168; Peptidase_C1.
InterPro; IPR000169; Thiolprot_act_site.
                                                                                                                                                                                                                                                                                                                          or send an
                                                                                                                                                                                                                                                                                                                                    entities
                                                                                                                                                                                                                                                                                                                                                                                                                    -I- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA.
-I- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS PAPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J; TISSUE-Embryo; MEDLINE-99456833; PubMed-10526153;
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                                                                                                                                                                                                                                                                           EMBL; AF158182; AAD41898.1; HSSP; P07711; 1CJL.
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16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        placenta-restricted expression.";
ett. 459:290-304/1000
                                                                                                                                                                    PS00640;
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                                                                                                                                                                  THIOL_PROTEASE_HIS;
THIOL_PROTEASE_ASN;
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Q929G5; Q9K1Y9; Q924H9;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=AR39;
MEDLINE=20150255; PubMed=10684935;
MEDLINE=20150255; PubMed=10684935;
Read T.D., Brunham R.C., Shen C., Gill S.R., Heidelberg
White O., Hickey E.K., Peterson J., Utterback T., Berry
Linher K., Weidman J., Khouri H., Craven B., Bowman C.,
Linher K., Weidman J., Kouri H., Craven J., McClarty G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstailor the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                             Shirai M., Hirakawa H., Kimoto M., Tabuchi M., Kishi F., Shiba T., Ishii K., Hattori M., Kuhara S., Nakazawa T.; Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Tonia T., Ton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Probable outer membrane protein pmpl precursor protein 1) (Outer membrane protein 6). PMPl OR OMP6 OR CPN0005 OR CP0770.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Christiansen G., Boesen T., Hjerno K.,
Madsen A.S., Knudsen K., Falk E., Birk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chlamydia pneumoniae (Chlamydophila pneumoniae)
Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
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                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-20330349; PubMed-10871362;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Genome sequences of Chlamydia trachomatis pneumoniae AR39.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=83558;
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leic Acids Res. 28:2311-2314(2000)
SUBCELLULAR LOCATION: CELL WALL S
                                                                                                                                                                                        SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY
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                                                                                                                                                                                                                       (POTENTIAL).
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M., Nelson W., DeBoy R., Ko
J., Fraser C.M.;
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37147 MW;
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Birkelund S.;
                                                                                                                                                                                                                                                SURFACE (ELEMENTARY
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nodson R.,
harg S.L.,
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01-FEB-1995 (Rel. 31, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pollen allergen Zea m 1 (Zea m I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRINTS; PR01225; EXPANSNFAMĒY.
PRODOM; PD002179; PO11en_allergen; 1.
PROSITE; PS50843; EXPANSIN_EB45; 1.
PROSITE; PS50842; EXPANSIN_EB45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Q07154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Allergen; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MaizeDB; 65840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HSSP; P43214; 1WHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=94010312; PubMed=8406014;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; L14271; AAA33496.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -!- DEVELOPMENTAL STAGE: EXPRESSION LOW BEFORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rye grass.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bedinger P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Broadwater A.H., Rubinstein A.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TISSUE=Pollen;
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206 PPTWSFGQTYTGG-QF
                                                                                    116 DDGDIVLMEIQDKLSAEWKPMKLSWGAIWRMDTAKALKG-PFSIRLTSESGKKVIAKDII 174
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALL SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CGB DOMAIN. SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 131:227-230(1993).
TISSUE SPECIFICITY: POLLEN TISSUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DISEASE: CAUSES MAIZE POLLEN ALLERGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        POLLEN MITOSIS
                                                                                                                                          GAGDVHSVSMKGS-RTKWQLMSRNWGQNWQSNS--YLNGQSLSFVVTTSDRRSVVSFNVA
                                                                                                                                                                                                   GKAFGSLAKPGLNDKLRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGCNPNYVAVLVKFVA
                                                                                                                                                                                                                                                            QPIYEKIA-----LYKSGIIPVMYRRVRCKRSGGIRFTINGHSYFN----LVLVTNVG
                                                                                                                                                                                                                                                                                                                     TACGNVPIFKDGKGCGSCYEVRCKEKPECSGNPVTVFITDMNYEPIA-----PYHFDLS
                                                                                                                                                                                                                                                                                                                                                                              TAALSTALFDQGLSCGACXELMCVNDPQWCIKGRSIVVTATNFCPPGGACDPPNHHFDLS
                                                                                                                                                                                                                                                                                                                                                                                                                                          l Similarity
53; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      L524; JC1524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the maize homolog of the allergen-encoding Lol pI gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   105
191 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21362 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  14.8%;
27.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                          33;
                                                                                                                                                                                                                                                                                                                                                                                                                              Score 178; DB 1; ... Pred. No. 5.1e-10; ...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EXPANSIN-LIKE EG45. EXPANSIN-LIKE CBD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6E2A9DF921C45C63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chay C.H., Klapper D.G.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AND HIGH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 191;
                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                       22;
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DISULFID
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                           Pfam; PF00734; CBD_1; 1.
Pfam; PF02015; Glyco_hydro_45; 1.
ProDom; PD001821; CBD_fungal; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                         PROSITE; PS00562; CBD_FUNGAL; 1.
PROSITE; PS50842; EXPANSIN_EG45; 1.
PROSITE; PS01140; GLYCOSYL_HYDROL_F45;
                                                                                                                                                                                                                                                                                                                                                 ProDom; PD001821; CBD; SMART; SM00236; fCBD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase (Cellulase V) (EG V).
                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR000254; CBD_fungal.
InterPro; IPR000334; Glyco_hydro_45.
                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; Z33381; CAA83846.1; -. HSSP; P00725; 2CBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linkages in cellulose.
-i- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mol. Microbiol. 13:219-228(1994).
-i- CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=QM9414 / RUT C-30;
MEDLINE=95075308; PubMed=7984103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypocreales; Hypocreaceae; Hypocrea.
NCBI_TaxID=51453;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Trichoderma reesei (Hypocrea jecorina).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GUN5_TRIRE
                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                               Cellulose
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        isolated by expression
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P43317;
01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A novel,
55 GACXELM-----CVNDPQWCIKGRSIVVTATNFCPPGGACD---
                                         20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      HYDROLASES).
SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
                                                                  AHATFYXXGDAXXTMGGACGYGNLYSQ------GYGLETAALSTALFDQ------GLSC
                                                                                                         Similarity
                                                                                                                                                                                                                                                                                   degradation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         small endoglucanase gene, egl5, from by expression in yeast.";
                                                                                             Conservative
                                                                                                                                                 AA;
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                                                                                                                                                                         242
134
182
205
242
182
230
                                        -GACGCGSSSGAFPWQLGIGNGVYTAAGSQALFDTAGASWCGAGC 74
                                                                                                        9.0%;
                                                                                                                                                 24411 MW;
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                                                                                             9;
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Pred.
                                                                                                                                                              BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                               PRO/SER-RICH (LINKER).
CELLULOSE-BINDING (BY SIMILARITY).
                                                                                                                                                                                       N-LINKED (GLCNAC. .
                                                                                                                                                                                                                                          PROTON DONOR (BY SIMILARITY).
                                                                                                                                                                                                                                                       NUCLEOPHILE (BY SIMILARITY)
                                                                                                                                                                                                                                                                     ENDOGLUCANASE V.
                                                                                                                                                                                                                                                                                   POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                 CC033FC51326C71D CRC64;
                                                                                             Mismatches
                                                                                                          108.5;
No. 0.0
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                                                                                                            .0028;
                                                                                                                    DB 1;
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                                                                                             40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Trichoderma
                                                                                                                                                                                       .) (POTENTIAL)
                                                                                                                    Length
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             PPNHHFD
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CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS -i- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN. -i- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Identification of canary grass (Phalaris aquatica) pollen allergens by immunoblotting: IgE and IgG antibody-binding studies."; Allergy 48:273-281(1993).
                                                                                                                                                                                                                                                                                                                                   SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE; PS50843; EXPANSIN_CBD; 1. PROSITE; PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SÜBCELLULAR LOCATION: Secreted.
-1- DISEASE: CAUSES GRASS POLLEN ALLERGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Phalaris aquatica (Canary grass).

Embryophyta; Tracheophyta;

Embryophyta; Tracheophyta;

Embryophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Suphioglu C., Singh M.B., Simpson R.J., Ward L., Knox R.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-93319091; PubMed-7687099;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=96105569; PubMed=8564724;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR000882; Pollen_allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Clin. Exp. Allergy 25:853-865(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Cloning, sequencing and expression in Escherichia coli of Pha a 1 and four isoforms of Pha a 5, the major allergens of canary grass
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Suphioglu C., Singh M.B.;
216 IELKESWGAIWRIDTPDKLTG---PFTVRYTTEGGTKAEFEDVIPEGW
                                                                                                                                    107
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                                                                                                                                                                                                                                                                                    Local
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                                 QLMSRNWGQNWQSNS--YLNGQSLSFVV--TTSDRRSVVSFNVAPPTW
                                                                                                SGIIPVMYRRVRCKRSGGIRFTIN----GHSYFNLVLVTNVGGAGDVHSVSMK-GSRTKW 165
                                                                                                                                                                                                  WLDAKSTWYGKPTGAGPKDNGGACGYKDVDKAPFNGMTGCGNTPIFKDGRGCGSCFELKC 106
                                                              AGELELQFRRVKCKYPDGTKPTFHVEKGSNPNYLALLVKYVDGDGDVVAVDIKEKGKDKW
                                                                                                                                                                VNDPQWCIKGRSIVVTATN-----FCPPGGACDPPNHHFDLSQPIYEKIA-----LYK 110
                                                                                                                                 -SKPESC-SGEPITVHITDDNEEPIAP-----YHFDLSGHAFGSMAKKGEEENVRG 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PF01357; Pollen_allergen;
S; PR01225; EXPANSNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P43214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S80654; AAB35984.1; -.
                                                                                                                                                                                                                                                                    65; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD002179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          non-profit
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1WHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                   29011
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         institutions as long as its content
                                                                                                                                                                                                                                                                                16.8%;
28.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Signal.
                                                                                                                                                                                                                                                                                                                                     MW.
                                                                                                                                                                                                                                                                    36;
                                                                                                                                                                                                                                                                                                                                                 MAJOR POLLEN ALLERGEN PHA A 1.
EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC...) (POTENT
P -> G (IN REF. 2).
                                                                                                                                                                                                                                                                                  Score 202.5;
Pred. No. 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             the major allergens of canary grass
                                                                                                                                                                                                                                                                                                                                   05883A458ACE877F CRC64;
                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                  .4e-12
                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                               . .) (POTENTIAL).
                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                Length
260
                                                                                                                                                                                                                                                               37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pooideae;
                                                                                                                                                                                                                                                                 Gaps
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                                                                                                                                                                                                                                                          RESULT 6
MPO1_ORYSA
                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MPO1_ORYSA STANDARD;
Q40638;
O1-NOV-1997 (Rel. 35, Created)
O1-NOV-1997 (Rel. 35, Last seq
O1-MAR-2002 (Rel. 41, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -i- TISSUE SPECIFICITY: EXPRESSED IN MATURE ANTHERS I VEGETATIVE OR OTHER FLORAL TISSUES.
-i- DISEASE: CAUSES GRASS POLLEN ALLERGY.
-i- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLI-
-i- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-i- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Cloning, expression and immunological characterization of Ory s the major allergen of rice pollen."; Gene 164:255-259(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Traci Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae, Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Major pollen allergen Ory s 1 precursor Oryza sativa (Rice).
                                                                                                                                                                                                                                                          SEQUENCE
                                                                                                                                                                                                                                                                                                                             SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; U31771; AAA86533.1; -. HSSP; P43214; IWHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                       CARBOHYD
                                                                                                                                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                  DOMAIN
                                                                                                                                                                                                                                                                                                                                          Allergen;
                                                                                                                                                                                                                                                                                                                                                           PROSITE;
                                                                                                                                                                                                                                                                                                                                                                      PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD002179;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -!- TISSUE SPECIFICITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bhalla P.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=96069591; PubMed=7590339;
                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=4530;
                                                        135
                                                                                    119
                                                                                                               81
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                                                                                                                                            61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Secreted
                                                                                                                                                                   GGACGYGNLYSQGY-GLETAALSTALEDQGLSCGACXELMCVNDPQWCI-KGRSIVVTAT 80
 LSFVVTTSDRRSVVSFNVAPP 207
                                                                                                                                         GGACGYKDVDKAPFLGMNSCG-NDPIFKDGKGCGSCFEIKC-SKPEACSDKPALIHVTDM 1.18
                            IEKASNPNYLALLVKYVAGDGDVVEVEIKEKGSE-EWKALKESWGAIWRIDTPKPLKGPF
                                                                                                           NFCPPGGACDPP--NHHFDLSQPIYEKIA----LYKSGIIPVMYRRVRCKRSGGIRFTIN 134
                                                                                                                                                                                                   63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Theerakulpisut P.,
                                                                                                                                                                                                                                                                                                                    PS50843; EXPANSIN_EG45; 1.
PS50842; EXPANSIN_EG45; 1.
POTENTIAL.
                                                                                                                                                                                                                Similarity
                                                    GHSYFNLVLVTNVGGAGDVHSVSM--KGSRTKWQLMSRNWGQNWQSNS--YLNGQS
                                                                                                                                                                                                                                                                                                                                                                                                                              IPR000882; Pollen_allergen.
                                                                                                                                                                                                                                                          263 AA;
                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                         24
61
178
32
                                                                                   -DEPIAAYHFDLSGLAMAKDGKDEELRKAGIIDTQFRRVKCKYPADTKITFH
                                                                                                                                                                                                                                                                                                                                                                     Pollen_allergen; 1. EXPANSIN_CBD; 1.
                                                                                                                                                                                                                                                                         263
164
259
32
                                                                                                                                                                                                                                                          28497
                                                                                                                                                                                                                15.7%;
31.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Goulding N.,
                                                                                                                                                                                                 29;
                                                                                                                                                                                                             Score 188.5;
Pred. No. 7.
                                                                                                                                                                                                                                                                    N-LINKED (GLCNAC
                                                                                                                                                                                                                                                                                                MAJOR POLLEN ALLERGEN EXPANSIN-LIKE EG45.
                                                                                                                                                                                                                                                                                   EXPANSIN-LIKE CBD.
                                                                                                                                                                                                                                                        B1C5F24EA398DD60 CRC64;
                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ormatics and the EMBL outstation There are no restrictions on it on as its content is in no wa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Suphioglu C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Ory s
                                                                                                                                                                                                                . 2e-11;
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                                                                                                                                                                                                                          DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Usage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OF ALLERGENS DOMAIN.
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                                                                                                                                                                                                                                                                      (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Tracheophyta;
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                                                                                                                                                                                                                                                                                                        1_HOLLA STANDARD MPH1_HOLLA STANDARD P43216; Q39975; O1-NOV-1995 (Rel. 32, L O1-NOV-1995 (Rel. 32, L O1-MAR-2002 (Rel. 41, L O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR;
                       Schramm G.D., Bufe A., Becker W.M., SCHLdan R., Submitted (NOV-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                        Holcus lanatus (Velvet grass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                            STRAIN-CV. AVENEAE; TISSUE-Pollen; Schramm G.D., Bufe A., Becker W.M., Schlaak M.;
                                                                                                                                                                            Poeae; Holcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CHAIN
SEQUENCE OF 18-265 FROM N.A.
                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                     NCBI_TaxID=29679;
                                                                                                                                                                                                                                                                                          Major
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000882; Pollen_allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HSSP; P43214;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 IELKESWGAVWRIDTPDKLTGPFTVRYTTEGGTKSEFE-DVIPEGWKADTSYS
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S13614; S13614.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QLMSRNWGQNWQSNS--YLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AGELELQFRRVKCKYPDDTKPTFHVEKASNPNYLAILVKYVDGDGDVVAVDIKEKGKDKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SGIIPVMYRRVRCKRSGGIRFTINGHSYFN----LVLVTNVGGAGDVHSVSMK-GSRTKW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WLDAKSTWYGKPTGAGPKDNGGACGYKNVDKAPFNGMTGCGNTPIFKDGRGCGSCFEIKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WINAHATEYX--XGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VNDPQWCIKGRSIVVTATN-----FCPPGGACDPPNHHFDLSQPIYEKIA------LYK 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 M57474; AAA63279.1; M57476; AAA63278.1;
                                                                                                                                                                                                                                                                                        pollen allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PS50843;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AA;
                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pollen_allergen; 1.
EXPANSIN_CBD; 1.
EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           263
167
262
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27.5%;
                                                                                                                                                                                                                                                                                          Hol l 1 precursor (Hol l I) (Hol l 1.0101
                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                         Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC...
N-> D.
A-> G.
A-> G.
I-> T.
F-> V.
P-> C (IN REF. 3).
P-> C (IN REF. 3).
P-> WW (IN REF. 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 215.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      POLLEN ALLERGEN LOL P 1.
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7675896F279C88C9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ed. No. 1.9e-13;
Mismatches 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                          265
                                                                                                                                                                                                                                                                                                                                                                                                          ΑA
                                                                                                                                                                                                    Poales; Poaceae; Pooideae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 263;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        261
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RESULT
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Best Local
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MPA1_PHAAQ STANDARD; PRT; 269 (041260; 01-NOV-1997 (Rel. 35, Created) 01-NOV-1997 (Rel. 35, Last sequence upda 01-MAR-2002 (Rel. 41, Last annotation up Major pollen allergen Pha a 1 precursor
                                                                                                                                                                                                                                                                                                                                                                                                                             DOMAIN
VARIANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Z27084; CAA81610.1; -. EMBL; Z68893; CAA93121.1; -. HSSP; P43214; 1WHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       between the Swiss Institute of Bioinformatics and the E the European Bioinformatics Institute. There are no rest use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Schramm G.D., Bufe A., Petersen A., Haas H., Schlaak M., Becker "Mapping of IgE-binding epitopes on the recombinant major group allergen of velvet grass pollen, rHol 1 1 "; J. Allergy Clin. Immunol. 99:781-787(1997).
                                                                                PHAAQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR000882; Pollen_allergen
pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CHARACTERIZATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CV. AVENEAE; TISSUE=Pollen; MEDLINE=97358126; PubMed=9215246;
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_aller
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=96319506; PubMed=8768803;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PROSITE; PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE; PS50843;
                                                                                                                                        212
                                                                                                                                                                                                                                                 103 TK-PESC-SGEPVTVHITDDNEEPIAP
                                                                                                                                                                                                                                                                          63 VNDPQWCIKGRSIVVTAIN-----FCPPGGACDPPNHHFDLSQPIYEKIA-----LYK
                                                                                                                                                                                                                                                                                                     43 WLDAKSTWYGKPTGAGPKDNGGACGYKDVDKPPFSGMTGCGNTPIFKDGRGCGSCFEIKC
                                                                                                                                                                                                                                                                                                                                5 WINAHATFYX--XGDAXXIMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC
                                                                                                                                        IELKESWGAVWRVDTPDKLTG----PFTVRYTTEGGTKGEAEDVIPEGWKADTAY
                                                                                                                                                                                                          SGIIPVMYRRVRCKRSGGIRFTIN----GHSYFNLVLVTNVGGAGDVHSVSMK-GSRTKW
                                                                                                                                                                QLMSRNWGQNWQSNS--YLNGQSLSFVV--TTSDRRSVVSFNVAPPTWSFGQTY
                                                                                                                                                                                            AGELELKFRRVKCKYPDGTKPTFHVEKGSNPNYLALLVKYIDGDGDVVAVDIKEKGKDKW
                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                265 AA;
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63
183
103
                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pollen_allergen; EXPANSIN_CBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                             25
265
169
264
103
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                                                                                                                                                                                                                                                                                                                                                                                                                 28590
                                                                                                                                                                                                                                                                                                                                                                        17.1%; Score 205.5; DB 1 27.4%; Pred. No. 1.7e-12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       MAJOR POLLEN ALLERGEN HOL L EXPANSIN-LIKE EG45.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                 -> S (IN HOL L 1.0102).
1FE23B3EE198AD6D CRC64;
                                                                                                                                                                                                                                                                                                                                                             Mismatches
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                          update)
                                                                      269
                                                                                                                                                                                                                                                    ---YHFDLSGHAFGSMAKKGEEQKLRS
    (Pha
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    a I).
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                                                                                                                                                                                                                                                                                                                                                                                     Length 265;
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MPC1_CYNDA
                               Query Match
Best Local
           Matches
                                                                                                                     CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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004701;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cynodon dactylon (Bermuda grass).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC cl
Chloridoideae; Cynodonteae; Cynodon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Major pollen allergen Cyn d 1.
                                                                                                                                                                      DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; S83343; AAB50734.2; -. HSSP; P43214; 1WHO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Singh M.B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Smith P.M., Suphioglu C., Griffith I.J., Theriault K., Knox R.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE-Pollen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                                                                                                             Allergen.
                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Singh M.B.;
"Cloning and expression in yeast Pichia pastoris of a biologically
active form of Cvn d 1, the major allergen of Bermuda grass pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-96347957; PubMed-8757211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CYND1
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                                                                                                                                                                                                                                                                                                                                                      PF01357; Pollen_allergen. 1.
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                                                                                                                                                                                                                                                                              PR01225; EXPANSNFAMLY PD002179; Pollen_alle; PS50843; EXPANSIN_CB
                                  Similarity
                                                                                                                                                                                                                                                    PS50842; EXPANSIN_EG45; 1.
                                                                                                                  246 AA;
        Conservative
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                                                                                                                                                                                                                                                                              Pollen_allergen; 1. EXPANSIN_CBD; 1.
                                                                                                                                               145
240
9
                                                                                                                  26888
                            17.9%;
28.1%;
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        37;
                            Score 216;
Pred. No. 1.
                                                                                                             EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC. . .) (P
43D8442DBA588322 CRC64;
     Mismatches
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                               .6e-13;
                                                         DB 1;
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                                                   Length 246;
  Indels
                                                                                                                                       (POTENTIAL).
  36;
Gaps
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           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                - I SUBCELLULAR LOCATION: Secreted.
- I DISEASE: CAUSES GRASS POLLEN ALLERGY.
- I SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS
- I SIMILARITY: CONTAINS 1 EXPANSIN-LIKE E645 DOMAIN.
- I SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           p14946; p19964;
01-APR-1990 (Rel. 14, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pollen allergen Lol p 1 precursor (Lol p I) (Allergen R7).
Lolium perenne (Perennial ryegrass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                            Esch R.E., Klapper D.G.;
"Isolation and characterization of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=90375479; PubMed=1697854;
Perez M., Ishioka G.Y., Walker L.E., Chesnut R.W.;
"cDNA cloning and immunological characterization o
                                                                                                                                                                                                                                                                                                      Biochem. J. 234:305-310(1986).
                                                                                                                                                                                                                                                                                                                        proteins from rye-grass (Lolium perenne) pollen prepared by a rapid
and efficient purification method.";
                                                                                                                                                                                                                                                                                                                                                    Cottam G.P., Moran D.M., Standring R.; "Physicochemical and immunochemical characterization of allergenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griffith I.J., Smith P.M., Pollock J., Theerakulpisut Avjoglu A., Davies S., Hough T., Singh M.B., Simpson I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _LOLPR
                                                                                                                                                                                             I allergenic determinant
                                                                                                                                                                                                                                                   MEDLINE=89364850; PubMed=2475768;
                                                                                                                                                                                                                                                                    SEQUENCE OF 236-263
                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=86242068; PubMed=3718469;
                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=Pollen;
                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 24-53.
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CYSP_SCHMA
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| 4 . ZZ0000 · ·                                                                                                                    | OT entry is copyrig<br>Swiss Institute of<br>Bioinformatics Inst<br>profit institution<br>this statement is<br>nires a license agre                                    | EPOllen; EPOllen; EPOllen; E-95015525; PubMed-79 S., Valenta R., Vrta er O., Duchene M.; ementary DNA cloning (Phleum pratense); ref I allergens from eigh ergy Clin. Immunol. 9 BCELLULAR LOCATION: S MILARITY: BELONGS TO MILARITY: CONTAINS 1 MILARITY: CONTAINS 1 | Distance by                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | STANDARD;               | 491<br>1246<br>1038<br>2491<br>3010<br>480<br>1004<br>319<br>308<br>502<br>561                                                      |
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YOO S.-D., Gao Z., Cantini C., Loescher W., van Nocker S.;
"Coordinated expression of genes encoding expansins and other cell wall-modifying enzymes is associated with pectin-related changes in the cell wall during ripening of cherry (P. cerasus) fruit.";
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF297521; AAG13982.1;
EMBL; AF350937; AAK48846.1;
EMBL; AF350937; AAK48846.1;
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PRINTS; PR0125; EXPANSNEAMLY.
PRODOm; PD002179; Pollen_allergen; 1.
SEQUENCE 254 AA; 27278 MW; 953A7EB2491FD0E1 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Prunus cerasus.

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Rosales; Rosaceae; Amygdaloideae; Prunus.
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01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                              175 NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Differential Expression of Expansin Genes Isolated from Sweet Cherry (Prunus avium L.) During Fruit Ripening."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
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Wu Z., Wiersma P.A.;
                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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EXP1 OR EXP2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                NWQSNTYLNGQSLSFQVTTSDGRTVTNYNVAPGNWQFGQTFSGGQF 254
                                                                                                                                                                                                                                                                                                                                                                                                                              VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                   PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                                                                                                                                                                                                                                                                  GGWEGAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGSCYEMRC 89
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161; Conservative 23; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     73.9%; Score 889.5; DB 1
71.2%; Pred. No. 3.2e-82;
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RESULT 12
Q93XP1
RESULT 13
08209
1D 08209
AC 08209
AC 08209
AC 01-NC
DT 01-NC
DT 01-DE
EXPAN
GN PA-EX
OS Prunu
OC Eukaz
OC Sperm
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid
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                              Prunus armeniaca (Apricot).
Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YOO S.-D., van Nocker S.; Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases EMBL; AF350938; AAK48847.1; -.
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01-DEC-2001
          Spermatophyta;
                                                                                                      EXPANSIN.
                                                                                                                             01-NOV-1998
01-DEC-2001
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TISSUE-FRUIT ABSCISSION ZONE;
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                                                                                PA-EXP1.
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                                                                                                                                                                                                                                                                                                                                            NWQSNSYLNGQSLSFKVTTSDGRTVVANNVAPACWSFGQTFSGVQF
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(TrEMBLrel. 19, Last sequence update)
(TrEMBLrel. 19, Last annotation update)
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                                                                                                                                                                                                                            PRELIMINARY;
          Magnoliophyta;
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26397 MW; C65556B038AB99D0 CRC64;
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Pred. No. 6e-83;
                                                                                                                                                                                                                            PRT;
            eudicotyledons;
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          Embryophyta; Tracheophyta;
edons; core eudicots; Rosid
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            Rosidae
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                                                                                                       Wrobel R.L., Yoder J.I.;
Wrobel R.L., Yoder J.I.;
Wrobel R.L., Yoder J.I.;
Wrobel R.L., Yoder J.I.;
"Differential RNA expression of alpha-expansin gene parasitic angiosperm Triphysaria versicolor (Single 266.85-93.(2001).

EMBL, AF330278; AAF32411.1; -...
InterPro; IPR000882; Pollen_allergen.

PRIMTS; PR01025; EXPANSWPAMLY.

PRODOM; PD002179; Pollen_allergen; 1.
SEQUENCE 249 AA; 26116 MW; DC976FEE376794FF CR
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Best Local
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                                                        Matches
                                                                                   Query Match
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Q9M515; O1-OCT-2000 (TremBLrel. 15,
01-OCT-2000 (TremBLrel. 15,
01-DEC-2001 (TremBLrel. 19,
                                                                                                                                                                                                                                                                                                                Triphysaria versicolor.
Eukaryota; Viridiplantae; Stre
Spermarophyta; Magnoliophyta;
Asteridae; euasterids I; Lamia
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STRAIN-BERGERON; TISSUE=MESOCARP PLUS EXOCARP;
Mbcguie-A-Mbeguie D., Gomez R.-M., Fils-Lycaon B.;
"Mclacular cloning and nucleotide sequence of expansin 1 (PA-Exp1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eurosids I; Rosales; NCBI_Tax1D=36596;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Molecular cloning and nucleotide sequence
from apricot fruit.";
                                                                                                                                                                                                                                                          TISSUE=ROOTS TREATED WITH DMBQ;
                                                                                                                                                                                                                                                                                                                                                                          ALPHA-EXPANSIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM
                                                                                                                                                                                                                                           MEDLINE=21186069; PubMed=11290422;
                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  NCBI_TaxID=64093;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000882; Pollen_allergen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209
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  23
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                                                                       Local
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                VNDPQWCIKGRSIVVTATNFCPP------GACDPPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NWQSNNYLNGQSLSFQVTTSDGRTVTSYNVAPGNWQFGQTFSGGQF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NNDPRWCRPG-SIIVTATNFCPPNFAQSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GGWEGAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGSCYEMRC
VGGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNSGLSCGSCYEIK
                                                        163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     162;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                       Similarity
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                                                        Conservative
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71.78;
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                                                                      74.18;
71.58;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosaceae; Amygdaloideae; Prunus
                                                                                                                                                                                                                                                                                                                    Lamiales; Orobanchaceae; Triphysaria
                                                                                                                                                                                                                                                                                                                             Streptophyta; Embryophyta; Tracheophyta; ta; eudicotyledons; core_eudicots;
                                                       23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22;
                                                                                                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 892.5;
Pred. No. 1.
                                                                      Score 892; DB 10;
Pred. No. 1.7e-82;
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88068D75932FD0E1 CRC64;
                                                          Mismatches
                                                                                                                 DC976FEE376794FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                 249
                                                                                   DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .6e-82;
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                                                          32;
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                                                                                                                                                                                                                 gene tamily members
                                                                                                                                                                                                  gene ramily members in (Scrophulariaceae).";
                                                                                     Length 249;
                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length
                                                           10;
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                                                        Gaps
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62 CVNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGI 113

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RESULT 10
Q9C554
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                                                   Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,

White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

RA Duehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dewar K.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Fright G.Y.,

RA Chung M.K., Conn L., Conway A.B., Conway A.R., Fright G.Y.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Kim C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Lin X., Liu S.X., Liu Z.A., Luros J.S., Maiti R., Marziali A.,

RA Militscher J., Miranda M., Nguyen M., Nierman W.C., Osborne B.I.,

RA Militscher J., Miranda M., Nguyen M., Rooney T., Rowley D.,

RA Sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

Sakano H., Tallon L.J., Tambunga G., Torimi M.J., Town C.D.,

Herterber J., Wen Alter G., William M.J., Town C.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M
Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bo
Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin
Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W.,
                 Utterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q9C554
Q9C554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CHAIN
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophytá; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21016719; PubMed=11130712;
                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Theologis A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
"Sequence and analysis of chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PUTATIVE EXPANSIN PROTEIN (AT-EXP1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGWINAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTAMFNNGLSCGSCFEIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      165;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length cDNA of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1
21
249
                                                                                                                                                                                                                                                                                                                                                                           COLUMBIA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     249 1
26597 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene F10D13_18 (GI:12597783).";
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73.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                       the EMBL/GenBank/DDBJ databases.
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Pred. No. 2.9e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ALPHA-EXPANSIN.
98F1D583B5E846CA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              POTENTIAL
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  1 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                250
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plant Arabidopsis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lin J.,
                                      Walker M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bowser L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ecker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Jones T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9;
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RESULT 11
080622
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Query Match
Best Local S
Matches 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local
                                                                                                                                                                                                                                                               STRAIN=CV. COLUMBIA;
MEDLING=20083487; Pubmed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
Cronin L.A., Shen M., Vanaken S.E., Umayam L., Tallon L.J., Gill J.E.,
Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
"Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nature 408:816-820(2000).
EMBL; AF360291; AAK26001.1; -.
EMBL; AC073178; AAG60095.1; -.
Interpro; IPR000882; Pollen_allergen.
PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
                                                            PRINTS; PRO1225; EXPANSNFAMLY.
PRODOM; PD002179; Pollen_allergen; 1
SEQUENCE 248 AA; 26482 MW; 29E31
                                                                                                                                            Submitted (MAR-2000) to the EMBL/GenBank/DDBJ EMBL; AC004138; AAC32927.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids II; Brassicales; Brassicaceae; Arabio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana (Mouse-ear cress). Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUTATIVE EXPANSIN.
AT2G03090.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1998 (TrEMBLrel. 01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  080622
                                                                                                            InterPro; IPR000882; Pollen_allergen
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                           STRAIN=CV.
                                                                                                                                                                                                                                                         thaliana.",
                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  080622;
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                                                                                                                                                                             Lin X.;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
                                                                                                                                                                                                                                             Nature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thaliana.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           85
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       63 VNDPQWCIKGRSIVVTATNFCPP-----GGACDPPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3 GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACYELMC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGWYNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        166;
                                                                                                                                                                                                                                          402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                              COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 08, (TrEMBLrel. 08, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Brassicales; Brassicaceae; Arabidopsis.
               75.4%;
72.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       75.5%;
73.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26518 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Created)
                            Score 907.5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 909.5;
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                                                               29E3199269B71271 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Embryophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AΑ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .9e-84;
                               DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 10;
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3
                                                                                                                                                             databases
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                               Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tracheophyta;
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Local Similarity mes 163; Conserv

Conservative

Pred. No. 4.6 4; Mismatches

.6e-84;

Indels

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Q38863;
01-NOV-1996 (TrEMBLrel. 01, Created)
                                     Q38863
                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PRO1225; EXPANSNFAMLY.
PRODOM: PD002179; Pollen_allergen; 1.
SEQUENCE 249 AA; 26428 MW; 63D014
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases EMBL; AC006535; AAR87031.1; ... EMBL; AF229437; AAF61712.1; -..
                                                                                                                    175 NMOSNSYLNGOSLSEVVTTSDRRSVVSENVAPPTWSEGOTYTGGOER 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Durachko D.M., Shcherban T.Y., Cosgrove D.J., "AtEXP10 is expressed in the trichomes, petic abscission zone.";
                                                                                                                                                             143 PVSYRRVPCRRRGGIRETINGHSYENLVLITNVGGAGDVHSAAIKGSRTVWQAMSRNWGQ 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AF229431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-CV.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JAN-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Connay A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Theologis A., Ecker J.; Lawsberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.;
                                                                                                                                                                                                        115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Cho H.,
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                                                                                                                                                                                                                                     84
                                                                                                                                                                                                                                                                  63
                                                                                                                                                                                                                                                                                 24 GGWINAHATFYGGGDASGTMGGACGYGNLYSQGYGTSTAALSTALFNNGLSCGSCFEIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expansin Atexp10 affects organ growth and morphology in Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                             3 GPWINAHATTFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC 62
                                                                                                    NWQSNSYLNGQALSFKVTTSDGRTVVSFNAAPAGWSYGQTFAGGQFR 249
                                                                                                                                                                         PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                                                                                                                       ENDGKWCLPG-SIVVTATNFCPPNNALANNNGGWCNPPLEHFDLAQPVFQRIAQYRAGIV 142
                                                                                                                                                                                                                                                  VNDPQWCIKGRSIVVTATNFCPP-----GGACDPPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cosgrove D.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      29431; AAF61713.1; -. IPR000882; Pollen_allergen.
                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COLUMBIA;
                                                                                                                                                                                                                                                                                                                                                               77.0%; Score 927.5;
73.6%; Pred. No. 4.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the trichomes, petioles, midribs, and pedicel
                                                                                                                                                                                                                                                                                                                                                  22;
                                                                                                                                                                                                                                                                                                                                                                                                         63D014410D4ABBA1 CRC64;
                                                                                                                                                                                                                                                                                                                                                Mismatches
                              237 AA.
                                                                                                                                                                                                                                                                                                                                                                4.3e-86
                                                                                                                                                                                                                                                                                                                                                                        DB 10; Length 249;
                                                                                                                                                                                                                                                                                                                                             29; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Matches 166;
     "Acid-growth response and alpha-expansins in suspension cultures bright yellow 2 tobacco."; Plant Physiol. 118:907-916(1998).

EMBL: AF049353; AAC96080.1; Interpro; IPR000882; Pollen_allergen.

Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                092P36 PRELIMINARY; PRT; 249 AA.
092P36; PRELIMINARY; PRT; 249 AA.
01-MAY-1999 (TrEMBLrel 10, Created)
01-MAY-1999 (TrEMBLrel 10, Last sequence up
01-DEC-2001 (TrEMBLrel 19, Last annotation
                                                                                                                                                                                                Eukaryota; Viridipiantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Nicotiana.
                                                                                                                                                                                                                                                     Nicotiana tabacum (Common tobacco)
                                                                                                                              MEDLINE=99026292; PubMed=9808735;
                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                              Link B.M., Cosgrove D.J.
                                                                                                                                                                                                                                                                               NT-EXP4.
                                                                                                                                                                                                                                                                                         ALPHA-EXPANSIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Shcherban T.Y., Shi J., Durachko D.M., Guiltinan M.J.,
McQueen-Mason S.J., Shieh M., Cosgrove D.J.;
"Molecular cloning and sequence analysis of expansins--a highly
conserved, multigene family of proteins that mediate cell wall
extension in plants.",
Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995).
InterPro: IPR000882; Polien_allergen.
Pram; PF0157; Pollen_allergen.
PRINTS; PR01225; EXPANSNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        191
                                                                                                                                                                                                                                                                                                                                                                                                                                                               175 NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosio
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=96016146; PubMed=7568110;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     72 QNDGKWCLPG-SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  63 VNDPQWCIKGRSIVVTATNECPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   12 GGWVNAHATFYGGGDASGTMGGACGYGNLYSOGYGTNTAALSTALFNNGLSCGACFEIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3 GPWINAHATEYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                            NWQSNSYLNGQSLSFKVTTSDGQTIVSNNVANAGWSFGQTFTGAQLR 237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 237 AA; 25155 MW; 0E5A2CB9C2943682 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
EXPANSNFAMLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.5%; Score 909.5; DB 1
73.1%; Pred. No. 2.7e-84;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19;
                                                                                                                                                                                                                                                                                                                    Last sequence update)
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9; Mismatches
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                                                                                                                                                                                                                                                                                                   update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9;
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Q9M517 5
Q9M517
ID Q9M5
AC Q9M5
D7 Q1-Q-D7 Q1-
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seQUENCE 252 AA; 26766 MW; 5C62EE
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pfam; PF01357; Pollen_allergen; 1.
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01-OCT-2000 (TrEMBLrel. 15, Last seq
01-DEC-2001 (TrEMBLrel. 19, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wrobel R.L., Yoder J.I.;
"Differential RNA expression of alpha-expansin gene family members in the parasitic angiosperm Triphysaria versicolor (Scrophulariaceae).";
Gene 266:85-93(2001).
GBBL; AF230276; AAF32409.1; -...
EMBL; AF230276; AAF32409.1; -...
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INTERPOS PRODOS PRINTS; PROJECTS; EXPANSWPAMLY.
PRODOM; PD002179; POLICE ALLEGEN; 1.
SEQUENCE 247 AA; 26456 MW; 0B2AC8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=64093;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PVAYRRVPCRRRGGIRFTINGHSYFNLVLITNVGGAGDVHSVSVKGSRTGWQAMSRNWGQ 205
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PVAYRRVACRRRGGIRFTINGHSYFNLVLVTNVGGAGDVHAVSIKGSRTGWQPMSRNWGQ
                                                                                                                                                                                                                                                                                         VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSOPIYEKIALYKSGII 114
                                                                                                                                                                                                                                                                                                                                                     GGWINAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTAMFNTGLSCGSCYEIRC 81
                                                        NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                    VNDGKWCLPG-SILVTATNFCPPNSALPNNAGGWCNPPLHHEDLAQPVFQHIAQYKAGIV 140
                                                                                                                                                PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
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73.68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77.2%; Score 929.5; DB 10; 74.4%; Pred. No. 2.7e-86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21; Mismatches
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0B2AC8F357CCF7B5 CRC64;
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RESULT 6
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Q9LDR9
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Spermatophyta; Magnoliophyta; edicotyledons; core eudicots; Asteridae; Asteridae; Asteridae; Asteridae;
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"Subcellular localization of expansin mRNA in xylem cells.";
plant Physiol. 123:463-470(2000).
EMBL; AF230333; AAF35902.1;
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PRINTS; PR01225; EXPANSNEAMLY.
PRODOM; PD002179; Pollen_allergen; 1.
SEQUENCE 242 AA; 26157 MW; 168A01724FCF5B58 CRC64;
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                                                                                                                                                                                                                                                                              01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
           Johnson-Hopson C., Dunn P., Brooks S., Buehler E., Chao Q., Khan S., Kim C., Shinn P., Altafi H., Bei Q., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzales A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Lee J., Lenz C., Li J., Liu A., Liu K., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thareri A., Toriumi M., Vaysberg M., Yu G., Federspiel N.A.,
                                                                                                                                                                                                                                                                                                                                                     Q9LDR9
                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                               T24P13.15 (EXPANSIN 10).
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                                                                                                                                                                                                                                Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                             eurosids
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Theologis A., Ecker J.R.;
                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       201 SYLNGOSLSFKVTTSDGRTVVSYNVAPSRWSFGQTFAGAQF 241
                                                                                                                                                         NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                82 VNDRQWCLPA-TIVVTATNFCPPNSNGGWCDPPRQHFDLSQPIFQHIAQYKAGVVPVAYR 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             63 VNDPQWCIKGRSIVVTATNFCPP---GGACDPPNHHFDLSQPIYEKIALYKSGIIPVMYR 119
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22 GGWSNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNKGLSCGSCYEIRC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSN 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQF 220
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                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                             Brassicales; Brassicaceae; Arabidopsis.
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76.0%;
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pred. No. 3.7e-86;
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Best 1
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Best Local 9
                                                                                                                                                                                                                                                                                                                            Matches
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Q9FNT1;
01-MAR-2001
01-MAR-2001
01-DEC-2001
                                                                                                                                                                                                                                                                                                                                                                                                        STRAIN-CV. CASTELLANA; TISSUE-ETIOLATED EPICOTYLS;
Dopico B., Sanchez M.A., Labrador E.;
"An expansin is expressed in chickpea epicotyls.";
submitted (DEC-2000) to the EMBL/GenBank/DDBJ datal
EMBL; AJ291816; CAC19183.1;
InterPro; IPR000882; Pollen_allergen.
PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF01357; Pollen_allergen; 1.
PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
SEQUENCE 255 AA; 27611 MW; 7580595A30DC414B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosid eurosids I; Fabales; Fabaceae; Papillonoideae; Cicereae; Cicer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Cicer arietinum (Chickpea)
                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EXPANSIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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                                                                                     185
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                                                                                                                                                                                                                                                                                                                                        Local
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                                                                                                                                                                                                                                                      WINAHATEYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALENNGLSCGACYEIKCYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           VRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNS
                                                                                   OSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFRY
                                                                                                                                                                                                        DPQWCIKGRSIVVTATNFCPPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVMYRRVRCK 124
                                                                                                                                                                                                                                                                                      WINNHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMCVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         HMGPWINAHATFYGGGDASGTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACFEL
                                                     QSLSFVVTTSNGHSVVSFNAAPSSWSFGQTYTGRQFNY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         YLNGOSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFRY 222
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MCVNDPQWCIKGRSIVVTATNFCPPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVMYRR 120
                                                                                                                      RKGGIRFTINGHSYFNLVLVTNVGGAGDVHSVAIKGSRSRWQAMSRNWGQNWQSNSTLNG
                                                                                                                                                                                        DPQWCIAGSSIVVTATNFCPPGGWCDPPNHHFDLSQPIFQQIAQYKARIVPVAYRRVRCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNS
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                                                                                                                                                                                                                                                                                                                             180;
                                                                                                                                                                                                                                                                                                                                            Similarity
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                                                                                                                                                                                                                                                                                                                                                                                           245 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (TrEMBLrel. 16, (TrEMBLrel. 16, (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                             26469 MW;
                                                                                                                                                                                                                                                                                                                                            83.3%;
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Last sequence
Last anno
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                                                                                                                                                                                                                                                                                                                                          Score 1003; DB 10
Pred. No. 9.2e-94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1195; DB 10;
Pred. No. 3.2e-113;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                           OEF6BFC835A38B23 CRC64;
                                                                                                                                                                                                                                                                                                                            Mismatches
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Best Local :
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01-MAR-2001
01-MAR-2001
01-DEC-2001
EXPANSIN 2.
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Q9ZP31;
01-MAY-1999
01-MAY-1999
01-DEC-2001
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SIGNAL
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                                                               SEQUENCE FROM N.A. Wu Z., Wiersma P.A.;
                                                                                                                                 Spermatophyta; Magnollophyta; eurosids I; Rosales; Rosaceae;
                                                                                                                                                                                                                                                                                                        Q9FUM2
                                                                                                                                                                     Eukaryota; Viridiplantae;
                                                                                                                                                                                     Prunus avium (Cherry).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ProDom; PD002179; Pollen_allergen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR01225; EXPANSNFAMLY.
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                                                                                                                   NCBI_TaxID=42229;
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239 .
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                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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239
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77.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25606 MW;
                                                                                                                                     Rosaceae;
                                                                                                                                                                                                                                      16,
19,
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                                                                                                                                                                                                                                                                                                        PRT;
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Wu Z., Wiersma P.A.; Differential Expression of Expansin Genes Isolated from "Differential Expression of Expansin Genes Isolated from (Prunus avium L.) During Fruit Ripening."; Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and ripening of tomato fruit.";
plant Wol. Biol. 39:161-169(1999).
EMBL; AF059489; AAD13633.1;
InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-CV. 91347; TISSUE=FRUIT;
STRAIN-CV. 91347; TISSUE=FRUIT;
MEDLINE=99178803; PubMed=10080718;
Brummell D.A., Harpster M.H., Dunsmuir P.;
"Differential expression of expansin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryoph
Spermatophyta; Magnoliophyta; eudicotyledons; cc
Asteridae; euasterids I; Solanales; Solanaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NGQSLSFVYTTSDRRSVVSENVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CRRSGGIRFTINGHSYFNLVLVTNVGGSGDVHSVYIKGSRTQWQPMSRNWGQNWQNNAYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQNWQSNSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VNDPQWCIKGRSIVYTATNFCPPGGACDPPNHHFDLSQPIYEKIALYKSGIIPVMYRRVR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       VNAGQYCLPG-IITVTATNECPPGGWCDPPRPHEDLSQPIELRIAQYRAGIVPVAYRRVP
                                                                                                                                                                  Streptophyta; Embryc
yta; eudicotyledons;
ceae; Amygdaloideae;
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Last annotation update)
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Last annotation update)
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Pred. No. 1e-
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                                                                                                                                                                                                            Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Embryophyta;
edons; core e
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                                                                                                                                                                        core eudicots;
Prunus.
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                                                                                                                                                                                             Rosidae;
                                                                           Cherry
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1.

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Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                        Database
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM protein - protein search, using sw model
   SPTREMBL_19:*
1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_invertebi:
6: sp_mammal:*
7: sp_mhc:*
8: sp_organell(
9: sp_bage:*
10: sp_plant:*
11: sp_rodent:
12: sp_virus:*
13: sp_vertebi:
14: sp_unclass:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result | Score | Query<br>Match | Length | DB | ID     | Description        |
|--------|-------|----------------|--------|----|--------|--------------------|
|        | 1195  | 99.3           | 255    | 10 | Q38864 | Q38864 arabidopsis |
| 2      | 1003  | 83.3           | 245    | 10 | Q9FNT1 | Q9fnt1 cicer ariet |
| ω      | 933.5 | 77.5           | 239    | 10 | Q9ZP31 | Q9zp31 lycopersico |
| 4      | 931.5 | 77.4           | 252    | 10 | Q9FUM2 | N                  |
| 5      | 929.5 | 77.2           | 247    | 10 | Q9M5I7 | Q9m5i7 triphysaria |
| 6      | 928   | 77.1           | 242    | 10 | Q9LLB1 | Q911b1 zinnia eleg |
| 7      | 927.5 | 77.0           | 249    | 10 | Q9LDR9 | Q9ldr9 arabidopsis |
| 80     | 909.5 | 75.5           | 237    | 10 | Q38863 | Q38863 arabidopsis |
| 9      | 909.5 | 75.5           | 249    | 10 | Q9ZP36 | Q9zp36 nicotiana t |
| 10     | 909.5 | 75.5           | 250    | 10 | Q9C554 | Q9c554 arabidopsis |
| 11     | 907.5 | 75.4           | 248    | 10 | 080622 | 080622 arabidopsis |
| 12     | 896.5 | 74.5           | 249    | 10 | Q93XP1 | Q93xpl prunus cera |
| 13     | 892.5 | 74.1           | 254    | 10 | 082093 | w                  |
| 14     | 892   | 74.1           | 249    | 10 | Q9M5I5 | Q9m5i5 triphysaria |
| 15     | 889.5 | 73.9           | 254    | 10 | Q9FUM3 | Q9fum3 prunus aviu |
| 16     | 886.5 | 73.6           | 245    | 10 | Q9LLB2 | Q911b2 zinnia eleg |
|        |       |                |        |    |        |                    |

| 118<br>122<br>122<br>122<br>122<br>122<br>123<br>124<br>125<br>126<br>127<br>127<br>127<br>127<br>127<br>127<br>127<br>127<br>127<br>127                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 17          |
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## ALIGNMENTS

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| Clones."; DNA Res. 7;131-135(2000). EMBL; U30478; AAB38071.1; EMBL; AB025615; BAA95756.1; InterPro; IPR000882; Pollen_allergen. | MAXABULE 1.; MAXABULE 1. Sequence "Structural analysis of Arabidopsis thaliana chromosome 3. 1. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC | SEQUENCE FROM N.A. STRAIN=COLUMBIA; MEDLINE=20277480; PubMed=10819329; | SEQUENCE FROM N.A. STRAIN=COLUMBIA; Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata S.; Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases. | conserved, multigene idmitly of proteins that mediate term warr extension in plants."; Proc. Natl. Acad. Sci. U.S.A. 92:9245-9249(1995). [2] | on CD CJ                              | Arabidopsis thaliana (Mouse-ear cress).  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;  eurosids II; Brassicales; Brassicaceae; Arabidopsis.  NCBI_TaxID-3702; | Q38864; 01-NOV-1996 (TrEMBLrel. 01, Created) 01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1996 (TrEMBLrel. 19, Last annotation update) EVPANSIN ATEX5 (EXPANSIN-LIKE PROTEIN). | LT 1<br>64<br>Q38864 PRELIMINARY; PRT; 255 AA. |

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06-MAY-1999
                                                                                                                                                                                                                                                                                                                 Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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30-APR-1999
31-AWY-1999
11-MAY-1999
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29-OCT-1999;
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| tandard; Protein; 253 AA.  0 (first entry)  s thaliana protein fragment SPQ ID NO: 27310.  s thaliana protein fragment SPQ ID NO: 27310.  s thaliana.  A2.  20.  2000EP-0301439.  9 99US-0123156. 9 99US-0123578. 9 99US-012358. 9 99US-012358. 9 99US-0123674. 9 99US-012466. 9 99US-0125024.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 196; Conservative 13; Mismatches 16; Indels 0; Gaps 0;  GWVNAHATFYGGGDASGTMGGACGYGNLYSOGYGTNTAALSTALFUNGLSCGACFEIRCQ 63                                                                                                                                             |
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| Identification; signal transduction pathway; metabolic pathway; ation assay; genetic mapping; gene expression control; promoter; i.on sequence.  15-A2.  15-A2 | entry)                                               | standard; Protein; 259 AA.                         |
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12; Mismatches
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.9e-106;
les 13;
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                                                          228
                                  259
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99US-0145183

17-OCT-2000 (first entry)

pathway;
promoter;

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RESULT 8
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9908-0154018
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9908-0155459
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9908-0157753
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89.0%;
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9908-0121825.
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| ק ק ק ק ק ק<br>ק ק ק ק ק                                                                     | 7 7 7 7                                         | PR                             | PR                             | PR                             | PR                             | 70 7          | R<br>R<br>R                   | PR                             | PR            | PR<br>R                        | PR            | g P                           | ים<br>אין     | D PR          | PR            | PR<br>R       | PR            |                               | בי<br>בי                       | PR            | P R                            | PR            | P R                  | PR            | PR<br>R                       | PR            | PR            | PR            | PR<br>B       | PR           | ק<br>ק       | PR           | д<br>ж       | PR           | ×             | PF X                 | PD ?              | PN            | 203           | X X X                                                                  |
|----------------------------------------------------------------------------------------------|-------------------------------------------------|--------------------------------|--------------------------------|--------------------------------|--------------------------------|---------------|-------------------------------|--------------------------------|---------------|--------------------------------|---------------|-------------------------------|---------------|---------------|---------------|---------------|---------------|-------------------------------|--------------------------------|---------------|--------------------------------|---------------|----------------------|---------------|-------------------------------|---------------|---------------|---------------|---------------|--------------|--------------|--------------|--------------|--------------|---------------|----------------------|-------------------|---------------|---------------|------------------------------------------------------------------------|
| 18-JUN-1999;<br>18-JUN-1999;<br>21-JUN-1999;<br>22-JUN-1999;<br>23-JUN-1999;<br>23-JUN-1999; | 18-JUN-1999;<br>18-JUN-1999;<br>18-JUN-1999;    | 18-JUN-1999;                   | 18-JUN-1999;                   | 18-JUN-1999;                   | 17-JUN-1999;<br>18-JUN-1999;   | 16-JUN-1999;  | 14-JUN-1999;                  | 10-JUN-1999;                   | 08-JUN-1999;  | 04-JUN-1999;                   | 03-JUN-1999;  | 28-MAY-1999;                  | 27-MAY-1999;  | 24-MAY-1999;  | 21-MAY-1999;  | 19-MAY-1999;  | 18-MAY-1999;  | 14-MAY-1999;                  | 14-MAY-1999;                   | 11-MAY-1999;  | 06-MAY-1999;                   | 06-MAY-1999;  | 04-MAY-1999;         | 30-APR-1999;  | 28-APR-1999;                  | 23-APR-1999;  | 21-APR-1999;  | 19-APR-1999;  | 08-APR-1999;  | 06-APR-1999; | 29-MAR-1999; | 25-MAR-1999; | 09-MAR-1999; | 05-MAR-1999; | 35-FFB-1000.  | 25-FEB-2000;         | 06-SEP-2000.      | EP1033405-A2. | Arabidopsis t | hybridisation<br>termination so                                        |
| 99US-0139763.<br>99US-0139817.<br>99US-0139899.<br>99US-0140353.<br>99US-0140354.            | 99US-0139461.<br>99US-0139462.<br>99US-0139463. | 99US-0139459.<br>99US-0139460. | 99US-0139457.<br>99US-0139458. | 99US-0139455.<br>99US-0139456. | 99US-0139492.<br>99US-0139454. | 9905-0139453. | 99US-0139119.<br>99US-0139452 | 99US-0138540.<br>99US-0138847. | 9905-0138094. | 99US-0137502.<br>99US-0137724. | 9908-0137528. | 99US-0136782.<br>99US-0137722 | 9905-0136392. | 99US-0135629. | 9908-0135353. | 9908-0134941. | 9905-0134768. | 99US-0134221.<br>99US-0134370 | 99US-0134218.<br>99US-0134219. | 9905-0134256. | 99US-0132487.<br>99US-0132863. | 9908-0132486. | 99US-0132484.        | 9908-0132407. | 99US-0131449.<br>99US-0132048 | 9905-0130891. | 99US-0130449. | 9905-0130077. | 99US-0128714. |              |              |              | 9US-(        | 12318        | 00115-0121825 | 2000EP-0301439.      |                   |               | thaliana.     | n assay; genetic mapping; gene expression control; promoter; sequence. |
|                                                                                              |                                                 |                                |                                |                                |                                |               |                               | -                              |               |                                |               |                               |               |               |               |               |               |                               |                                |               |                                |               |                      |               |                               |               |               |               |               |              |              |              |              |              |               |                      |                   |               |               |                                                                        |
| ק<br>אק<br>אק<br>אק<br>אק                                                                    | PR<br>PR                                        | PR                             | PR<br>PR                       | PR                             | PR<br>PR                       | PR            | PR                            | PR                             | PR            | PR<br>Rq                       | PR            | PR                            | PR            | PR            | PR            | PR            | PR            | PR                            | יט<br>א                        | PR            | PR<br>PR                       | PR            | PR                   | PR            | PR                            | PR            | PR            | PR            | PR            | PR           | PR           | PR           | PR           | יי<br>גער    | PR            | PR<br>R              | קר<br>קר          | יי<br>גענ     |               | קק<br>קק                                                               |
| 27-AUG-1999;<br>27-AUG-1999;<br>27-AUG-1999;<br>30-AUG-1999;<br>31-AUG-1999;<br>01-SEP-1999; | 1999                                            | 1999                           | 1999                           | -1999<br>-1999                 | -1999<br>-1999                 | 1999          | -1999<br>-1999                | 99                             | 9-AUG-1999    | -1999<br>-1999                 | 5-AUG-1999    | -1999                         | 4-AUG-1999    | -1999         | 2-AUG-1999    | 8-JUL-1999    | 1999          | -199                          | 99                             | 199           | 0.0                            | -199          | 0 10                 | 199           | 0 10                          | 199           | -199          | In I          | -199          | -199         | -199<br>-199 | -199         | ດທ           | -199         | -199          | ດເດ                  | 199<br>199<br>199 | 199           | 199           | 199                                                                    |
| 99US-0151065<br>99US-0151066<br>99US-0151080<br>99US-0151303<br>99US-0151438<br>99US-0151438 | 955                                             | 99                             | 20                             | 20                             | 20                             | 201           | 95                            | 20                             | 201           | င်္ပင်                         | 01            | 20                            | 01            | 20            | 01            | 95            | 01.           | 20                            | င်င်                           | 35            | 99                             | -01           | -0145085<br>-0145087 | 01            | -0144814<br>-0145086          | 01,           | 95            | 0144335       | 25            | 01.          | 95           | 01,          | 9            | 0143624      | 91            | -0142803<br>-0142920 | 0142390           | 01,           | 0141287       | -0140695<br>-0140823                                                   |

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07-OCT 1999
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11-OCT 1999
Protein identification; signal transduction pathway; metabolic pathway;
                 Arabidopsis thaliana protein fragment SEQ ID NO: 65569
                                                                          AAG51646
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9908-0155189
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9908-0160980
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12; Mismatches 13;
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114-OCT-1999
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114-OCT-1999
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114-OCT-1999
121-OCT-1999
                        Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
                                                         Arabidopsis
                                                                                         AAG51632;
                                                                                                         AAG51632 standard; Protein;
         Arabidopsis thaliana
                                                                        18-OCT-2000 (first entry)
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                                                       thaliana protein fragment SEQ ID NO: 65550.
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; Pred. No. 5.6e-106;
12; Mismatches 13;
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                                                                           Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
  25-FEB-2000; 2000EP-0301439
                     06-SEP-2000
                                       EP1033405-A2
                                                         Arabidopsis thaliana
                                                                                                                Arabidopsis thaliana protein fragment SEQ ID NO: 3356.
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5.3e-106;
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                                                        25-FEB-2000;
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                                                                                                                     Arabidopsis thaliana.
                                                                                                                                           termination sequence.
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  99US-0121825.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Expansin proteins which alter the mechanical strength of poly:saccharide(s) - useful in paper mfr. and recycling
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| is thali           | AAG23850 | 21 | 8      | æ      | 1115         |
| sis thali          | AAG43341 | 21 | 8      | 8.     | $\mathbf{L}$ |
| is thali           | 34       | 21 | S      | 8      | -            |
| opsis thal         | 23       | 21 | UΊ     | 8      | 1115         |
| Arabidopsis thalia | 4334     | 21 | S      | 8      | $\mathbf{H}$ |
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### ALIGNMENTS

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RESULT 1
AAR94528
      WPI; 1996-201150/21
                   Cosgrove DJ,
                                                                               04-APR-1996.
                                                                                            AU9540262-A
                                                                                                                Misc-difference
                                                                                                                       Key
                                                                                                                                    Oryza sativa
                               (PENN-) PENN
                                             12-MAY-1995;
12-MAY-1993;
                                                                 12-MAY-1994;
                                                                                                                                                  polysaccharide;
                                                                                                                                                        Expansin; plant cell wall; cellulose; paper recycling; de-inking;
                                                                                                                                                                     Rice expansin.
                                                                                                                                                                                   08-JUL-1996
                                                                                                                                                                                                AAR94528;
                                                                                                                                                                                                            AAR94528 standard; Protein;
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                   McQueen-Mason
                                STATE RES FOUND
                                              95US-0440517.
93US-0060944.
                                                                 94AU-0068320
                                                                                                                Location/Qualifiers
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                                                                                                          /note= "unidentified amino acid"
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CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 6
LENGTH: 179
TYPE: PRT
ORGANISM: Cucumis melo
US-09-362-642-6
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                                                                                                                                                                                                                                                                                                                                                              В
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Best Local S
Matches 137
                                                                                                                                                                                                                         Sequence 4, Application US/08440517A Patent No. 5959082 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6, Application US/09362642 Patent No. 6350935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches 137;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-07821005
                                                                                                                                               APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
APPLICANT: SHCHERBAN, TATYANA;
APPLICANT: SHI, JUN
                                                                                         TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               123 VPCRKQGGIRFTINGFRYFNLVLITNVAGAGDIVRVSVKGSNTGWMSMSRNWGQNWQ 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   128 VPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQNWQ 184
                                                                                                                                                                                                                                                                                                                                                            CITY:
STATE:
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nes 137; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                      63 HPGSPCIFITATNFCPPNFALPNDNGGWCNLPRTHFDLAMPMFLKIAEYRAGIGPVSYRR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63 HPGSPCIFITATNECPPNFALPNDNGGWCNLPRTHEDLAMPMELKIAEYRAGIGPVSYRR 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                            70 LPGS--IVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVPVAYRR 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 ATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRCQNDGKWC 69
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 77.4%; Pred. No. 3.1e-70;
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                                 ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY STREET: 113 TECHNOLOGY CENTER
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           14; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 4; Length 179;
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; NAME/KEY: UNSURE
; LOCATION: (2)..(227)
; OTHER INFORMATION: Xaa is unknown or other.
US-09-092-160-4
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                                                                                                                                                                                                               SEQ ID NO 4
LENGTH: 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
                                                                                                                                                                                                                                                                         EARLIER APPLICATION NUMBER: 08/440,517
EARLIER FILING DATE: 1995-05-12
EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS FILE REFERENCE: 1194/IC1140S3 CURRENT APPLICATION NUMBER: US/09/092,160C CURRENT FILING DATE: 1998-06-05
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Shcherban, Tatyana APPLICANT: Shi, Jun
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Ver. 2.1
                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis OTHER INFORMATION: expansin
                                                                                                                                                                     ORGANISM: Artificial Sequence
                                                                                    FEATURE:
                                                                                                                                                   FEATURE:
                                                                                                                                                                                             TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   184 QSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGW 216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      124 AYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGONW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               127 NYKRVPXQRSGGIRFAISGHDYFELVTVTNVGGSGVVAQMSIKGSNTGWMAMSRNWGANW
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        66 GKWCLPG--SIVYTATNECPPNNALPNNAGGWCNPPQQHEDLSQPVFQRIAQYRAGIVPV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Match 58.3%; Score 733.5; DB 2; Local Similarity 63.8%; Pred. No. 3.1e-66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/440,517A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    67 TKWCKPGGNSITITATNLCXPNWALPSNSGGWCNPPLXHFDMSQPAWENIAVYQAGIVPV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 NAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRCQ-ND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       136;
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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 225
; TYPE: PRT
; ORGANISM: Lycopersicon esculentum cv.
US-09-362-642-2
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US-09-362-642-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 2, Application US/08845539 Patent No. 5929303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Bennett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/362,642
CURRENT TILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 8
SOFTWARF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09362642 Patent No. 6350935
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Rose, Jocelyn K.C.
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: Fruit-Specific and Ripening Regulation Expansin Genes
TITLE OF INVENTION: to Control Fruit Texture and Softening
FILE REFERENCE: 023070-078210US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT:
APPLICANT:
                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation
TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
NUMBER OF SEQUENCES: 8
                    ATTORNEY/AGENT INFORMATION: NAME: Bastian, Kevin L.
                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       177 RNWGQNWQSNSYLNGQS 193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   209
                                                               CLASSIFICATION:
                                                                                   APPLICATION NUMBER: US/08/845,539 FILING DATE: 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89
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                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                 STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RNWGQNWQSNAVLTGQS 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAGIVPVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMS 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RAGIVPVTYRRIPCRKQGGIRFTINGFRYFNLVLITNVAGAGDIIKVWVKGTKTNWIALS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SGGSWETAHATFYGGSDASGIMGGACGYGNLYSQGYGVNTAALSTALFNNGLSCGACFEL 88
                                                                                                                                                                                                                                                           94111-3834
                                                                                                                                                                                                                                                                                                                        SSEE: Townsend and Townsend and Crew LLP
T: Two Embarcadero Center, Eighth Floor
San Francisco
                                                                                                                                                                                                                                                                                                        California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bennett, Alan
                                                                                                                                                                                                                                                                                  USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bennett, Alan B. Rose, Jocelyn K.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                 25-APR-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     66.8%; Score 841; DB 4; Length 225; 75.1%; Pred. No. 4.7e-77;
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; MOLECULE TYPE: US-08-845-539-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Applic Patent No. 5929303
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Matches 147; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (415) 576-030
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                               NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34.774
REFERENCE/DOCKET NUMBER: 02:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: TWO CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AMERAL INTURNAL....

APPLICANT: Bennett, Alan B.

APPLICANT: Rose, Jocelyn K.C.

TITLE OF INVENTION: Fruit-Specific and Ripening-Regulation

TITLE OF INVENTION: Expansin Genes to Control Fruit Texture and Softening
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: 02.
TELECOMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/08/845,539 FILING DATE: 25-APR-1997 CLASSIFICATION: 435
                                   TOPOLOGY:
                                                                                                                               TELEFAX:
                                                                         LENGTH:
                                                                                                                                                   TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCQN--DGKWCLPG--SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQY 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RAGIVPVTYRRIPCRKQGGIRFTINGFRYFNLVLITNVAGAGDIIKVWVKGTKTNWIPLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                              94111-3834
                                                   amino acid
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                                                                       179 amino acids
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                                                                                                                               (415) 576-0200
(415) 576-0300
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                                     linear
                                                                                                                                                                                                                                                                                                                                                              IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
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               protein
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74.68;
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SEQ ID NO 3
LENGTH: 222
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 5, Application US/08440517A Patent No. 5959082
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EARLIER APPLICATION NUMBER: 08/242,090
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
                                                                   FILING DATE:
CLASSIFICATION: 530
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: UNSURE LOCATION: (14)..(58
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                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: COSGROVE, DANIEL J.;
APPLICANT: GUILTINAN, MARK;
APPLICANT: SHCHERBAN, TATYANA;
APPLICANT: SHI, JUN
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: WORDPERFECT 5.1
CURRENT APPLICATION DATA:
                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         115
                                                                                                                                                                                                                                                                                                         ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, THE ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY STREET: 113 TECHNOLOGY CENTER CITY: UNIVERSITY PARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                                                                                                    COMPUTER: NEC 286
                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 114
TOPOLOGY: UNKNOWN
                                                                                                                           APPLICATION NUMBER: US/08/440,517A
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                                LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GGWVNAHATEYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALENNGLSCGACFEIRC 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSEGQTFTGAHVR 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NWQSNSYLNGQSLSEVVTTSDRRSVVSENVAPPTWSFGQTYTGGQFR 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GPWINAHATFYXXGDAXXTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACXELMC 62
                                                                                                                                                                                                                                                       TRY: UNITED STATES OF AMERICA
16802-7000
               AMINO ACID
                                                                                                                                                                                                                                                                                              PENNSYLVANIA
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; Pred. No. 7.6e-83;
19; Mismatches 35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID NO 5
LENGTH: 225
TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL
                                                                                                                                                                                                                                                                                                                                        Matches 154;
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                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/IC114US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 193-05-12
NUMBER OF SEO ID NOS: 7
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/09/092,160C CURRENT FILING DATE: 1998-06-05 EARLIER APPLICATION NUMBER: 08/440,517 EARLIER FILING DATE: 1995-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EARLIER APPLICATION NUMBER: 08/242,090 EARLIER FILING DATE: 1994-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: Description of Artificial Sequence: Arabidopsis OTHER INFORMATION: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FEATURE:
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                                                                                                                        123 VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTG-WQAMSRNWGQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        182 NWQSNSYLNGQSLSFKYTTSDGQTIVSNNXANAGWSFGQTFTG 224
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                                                                                                                                                                                                         63 QNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVP 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          63 QNDGKWCLPGSIVVTATNECPPNNALPNNAGGWCNPPQQHEDLSQPVFQRIAQYRAGIVP 122
                                                                                                                                                                                                                                                                        3 GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC
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NWQSNTYLRGQSLSFQVTDSDGRTVVSYDVVPHDWQFGQTFEG
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                                       NWQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTG 224
                                                                                   VAFRRVPCEKGGGIRFTINGNPYFDLVLITNVGGAGDIRAVSLKGSKTDQWQSMSRNWGQ
                                                                                                                                                                    EDDPEWCIPGSIIV----RYNLANFALANDNGGWCNPPLKHFDLAEPAFLQIAQYRAGIVP
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                                                                                                                                                                                                                                                                                                                                                         68.2%; Score 859; DB 4; 69.1%; Pred. No. 7.3e-79;
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Pred. No. 7.3e-79;
"'Amatches 37;
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LENGTH: 226
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/09092160C Patent No. 6255466
                                                                                                                                                                                                                                                                                                                  Matches 165;
                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: 08/
EARLIER FILING DATE: 1993-05-12
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/092,160C CURRENT FILING DATE: 1998-06-05 CARLIER APPLICATION NUMBER: 08/440,517 EARLIER FILING DATE: 1995-05-12 EARLIER APPLICATION NUMBER: 08/242,090 EARLIER FILING DATE: 1994-05-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 1194/1C114US3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
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184
                                    185
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                                                                                                                                                                                                                                                        WVNAHATTYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRCQN 64
SNSYLDGQSLSFQVAVSDGRTVTSNNVVPAGWQFGQTFEG 223
                                                                           YRRVPCVKKGGIRFTINGHSYFNLVLVTNVAGPGDVQSVSIKGSSTGWQPMSRNWGQNWQ 183
                                                                                                                YRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQNWQ 184
                                                                                                                                                      DGQWCLPGSVTVTATNLCPPNYALPNDDGGWCNPPRPHFDMAEPAFLQIGVYRAGIVPVS
                                                                                                                                                                           DGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVPVA 124
                                                                                                                                                                                                                                      WQSAHATFYGGGDASGTMGGTCGYGNLYSTGY-TNTAALSTVLFNDGAACRSCYELRCDN 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTG 224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             YRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQNWQ 184
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75.0%;
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                                                                                                                                                                                                                                                                                                                  23; Mismatches
                                                                                                                                                                                                                                                                                                                                    Score 959.5; DB 4; Pred. No. 5.6e-89;
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; Patent No. 5959082
US-09-092-160-3
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                                                                                                                                                                                                                                                                                                                                        Matches 164;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NUMBER OF SEQUENCES:
                                                                                    182 NWQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTGAHVR 228
                                                                   175 NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 221
                                                                                                                                    115 PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ 174
                                                                                                                                                    122 PVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQ 181
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                                                                                                                                                                                                     63 VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 114
                                                                                                                                                                                                                                   63 QNDGKWCLPG-SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV 121
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
                                                                                                                                                                                                                                                                     16802-7000
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                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SHCHERBAN, TATYANA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COSGROVE, DANIEL J.;
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APPLICANT: COSTIONE, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: McQueen-Mason, Simon
APPLICANT: Schierban, Tatyana
APPLICANT: Shi, Jun
APPLICANT: Shi, Jun
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/1C114US3
CURRENT APPLICATION NUMBER: US/09/092,160C
CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/440,517

; GENERAL INFORMATION:

Sequence 3, Application US/09092160C Patent No. 6255466

181 QNWQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTGAHVR 228

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US-09-092-160-2
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CURRENT FILING DATE: 1998-06-05
EARLIER APPLICATION NUMBER: 08/40,517
EARLIER FILING DATE: 1995-05-12
EARLIER FILING DATE: 1994-05-12
EARLIER FILING DATE: 1994-05-12
EARLIER APPLICATION NUMBER: 08/060,944
EARLIER FILING DATE: 1993-05-12
EARLIER FILING DATE: 1993-05-12
EARLIER FILING DATE: 1993-05-12
EARLIER FILING DATE: 1993-05-12
EARLIER FILING DATE: 1993-05-12
                                                                                                                                             Sequence 7, Application US/09092160C Patent No. 6255466 GENERAL INFORMATION:
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Patent No. 6255466
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APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
FILE REFERENCE: 1194/IC114US3
                                      APPLICANT: Cosgrove, Daniel J
APPLICANT: McQueen-Mason, Simon
APPLICANT: Guiltinan, Mark J
APPLICANT: Shcherban, Tatyana
APPLICANT: Shi, Jun
               APPLICANT: Shi, Jun
TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: UNSURE
LOCATION: 211
OTHER INFORMATION: Xaa is unknown or other.
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TYPE: PRT
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REFERENCE: 1194/1C114US3
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RESULT 4
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SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 7
LENGTH: 227
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                         CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO:
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                                                                                                                   COMPUTER: NEC 286
OPERATING SYSTEM: DOS
OPERARE: WORDDERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08,
                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
                                        SEQUENCE CHARACTERISTICS
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APPLICANT:
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APPLICANT: GUILTINAN, MARK;
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS NUMBER OF SEQUENCES: 6
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LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY
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                                                                                                    FILING DATE:
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SHI, JUN
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Maximum Match 100%
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1: /cgn2_6/ptodata/2/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
3: /cgn2_6/ptodata/2/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/iaa/FCTUS_COMB.pep:*
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                                                                                                                                                                                                Local c 228;
                     121 VPVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWG
                                                                        61
                                                                                                                                                                                                                                                                                                TOPOLOGY:
                                                                                                                                                                                                                                                                                                                 TYPE:
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                                                                                                                                        RCQNDGKWCLPGSIVYTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGI 120
       VPVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      286
                                                                                                                                                                                                           99.8%; Score 1257; DB 2;
100.0%; Pred. No. 6.5e-119;
Live 0; Mismatches 0;
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Result

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114 115 116 117 118 119 119 120 220 23 23 24 24 27

|            | 45               | 4 4               | 42                | 41                | 40                | 39                | 38                | 37                | 36                | 35<br>5           | 34                | S<br>S            | 32                | 31                | 30                | 29                | 28                |
|------------|------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|-------------------|
|            | 81               | 800               | ဆ ထ               | 83                | 83                | 83                | 83                | 83                | 97.5              | 97.5              | 97.5              | 97.5              | 101               | 152               | 154               | 154               | 191.5             |
|            | 6.4              | J (               | n 01              | 6.6               | 6.6               | 6.6               | 6.6               | 6.6               | 7.7               | 7.7               | 7.7               | 7.7               | 8.0               | 12.1              | 12.2              | 12.2              | 15.2              |
|            | 890              | 1160              | 1477              | 1477              | 1477              | 1477              | 1477              | 1477              | 145               | 145               | 145               | 145               | 54                | 122               | 200               | 197               | 245               |
|            | 20               | w.                | <b>~</b> N        | Ν                 | Ν                 | N                 | μ                 | ۳                 | 4                 | 4                 | 4                 | 4                 | ω                 | 4                 | 4                 | 4                 | 4                 |
| ALIGNMENTS | US-08-483-101-14 | US-08-808-599A-24 | US-08-617-697-4   | US-08-728-470-4   | US-08-469-880-4   | US-08-530-198-4   | US-08-302-832-4   | US-08-038-682-4   | US-08-174-739A-4  | US-08-433-288-4   | US-08-434-418-4   | US-08-413-974-4   | US-08-750-419A-12 | US-08-441-507-23  | US-08-441-507-4   | US-08-441-507-5   | US-08-441-507-24  |
|            | 14,              | 24,               | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 4, Appli | Sequence 12, Appl | Sequence 23, Appl | Sequence 4, Appli | Sequence 5, Appli | Sequence 24, Appl |

Title:

### Sequence 2, Application US/08440517A Patent No. 5959082 CLASSIFICATION: 530 INFORMATION FOR SEQ ID NO: OPERATING SYSTEM: DOS SOFTWARE: WORDPERFECT 5.1 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08, COMPUTER READABLE FORM: MEDIUM TYPE: FLOPPY DISK CORRESPONDENCE ADDRESS: SEQUENCE CHARACTERISTICS: TITLE OF INVENTION: PURIFIED EXPANSIN PROTEINS NUMBER OF SEQUENCES: 6 ADDRESSEE: INTELLECTUAL PROPERTY OFFICE, ADDRESSEE: PENNSYLVANIA STATE UNIVERSITY STREET: 113 TECHNOLOGY CENTER STREET: 113 TECHNOLOGY CITY: UNIVERSITY PARK RY: UNITED STATES OF 16802-7000 PENNSYLVANIA COSGROVE, DANIEL J.; GUILTINAN, SHCHERBAN, TATYANA; US/08/440,517A AMERICA

Length 228; Indels

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expansin EXP5 [imported] - Arabidopsis thaliana ("Species: Arabidopsis thaliana (mouse-ear cress) c;Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 28-Jul-2000 C;Date: 21-Jul-2000 C;Accession: T50655 C;Sccession: T50655 R;Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
C; Function:
A; Description: induces (
C; Superfamily: expansin
C; Keywords: cell wall
                                                                                                                                                                                                               A;Title: Molecular cloning and sequence analysis of A;Reference number: 214894; MUID:96016146 A;Accession: T50655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      R;Caderas, D.M. submitted to the EMBL Data Library, June 1999 A;Reference number: Z25160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expansin 9 [imported] - tomato
C;Species: Lycopersicon esculer
C;Date: 21-u1-2000 #sequence_I
C;Accession: T50658
                                                                            A; Gene: EXP5
                                                                                                C; Genetics:
                                                                                                                                      A; Cross-references: EMBL: U30478; PIDN: AAB38071.1
                                                                                                                                                       A; Molecule type: mRNA
A; Residues: 1-255 <SHC>
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C;Superfamily: expansin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-257 < CAD>
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A; Status: preliminary; translated
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                                                                                                                  A; Experimental source: variety
                                                                                                                                                                                           A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;Species: Lycopersicon esculentum (tomato);Date: 21-Jul-2000 #text_change 28-Jul-2000;Date: 21-Jul-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           179 WGQNWQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTGAHVR 228
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GIVPVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRN 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KCDNQPQWCHPGSPSILITATNFCPPNYALPNDNGGWCNPPRTHFDLAMPMFLKIAEYRA 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SGGSWQNAHATFYGGSDASGTMGGACGYGNLYSQGYGVNNAALSTALFNNGLSCGACFEI 86
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                                                                                                                    Columbia
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                                    (creep) in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 936; DB 2;
Pred. No. 7.8e-74;
3; Mismatches 39;
                                                                                                                                                                                               from GB/EMBL/DDBJ
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                                      plant cell walls
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Query Match

73 .98;

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930.5;

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Search completed: October Job time: 12.4421 secs

2002, 15:00:59

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expansin-like protein - Arabidopsis thaliana
N;Alternate names: protein T22E16.160
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 26-May-2000
C;Accession: T47689
R;Benes, V; Wurmbach, E.; Drzonek, H.; Ansorge, W.; Mewes, H.W.; Lemcke, K.
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C; Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                              A; Experimental source: cultivar Columbia; BAC clone T22E16 C; Genetics:
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A; Residues: 1-260 <BEN>
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A; Accession: T47689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the Protein Sequence Database,
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 210
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                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                       3 GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIKC
WGQNWQSNAVLVGQSLSFRVTSSDRRTSTSWNIAPSNWQFGQTFVGKNFR
                WGQNWQSNSYLNGQSLSFKYTTSDGQTIVSNNXANAGWSFGQTFTGAHVR 228
                                                                    GIVPISYRRVACRKSGGIRFTINGHRYFNLVLITNVAGAGDIARTSVKGSKTGWMSLTRN 209
                                                                                    GIVPVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRN 178
                                                                                                                                                      RCQNDGKWCLPG--SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRA 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NWQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTGAHVR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VNDPQWCIKGRSIVVTATNFCPP------GGACDPPNHHFDLSQPIYEKIALYKSGII 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         QNDGKWCLPG-SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GPWINAHATFYGGGDASGTMGGACGYGNLYSQGYGLETAALSTALFDQGLSCGACFELMC 95
                                                                                                                                    KCVNDPKWCHPGNPSVFVTATNFCPPNLAQPSDNGGWCNPPRSHFDLAMPVFLKTAEYRA 149
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NWQSNSYLNGQSLSFVVTTSDRRSVVSFNVAPPTWSFGQTYTGGQFR 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PVMYRRVRCKRSGGIRFTINGHSYFNLVLVTNVGGAGDVHSVSMKGSRTKWQLMSRNWGQ
                                                                                                                                                                                                                                                                             165;
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                                                                                                                                                                                                                                                                                             Similarity
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                                                                                                                                                                                                                                                                                               73.8%;
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.9; Mismatches 30;
                                                                                                                                                                                                                                                                                             Score 929; DB 2; Pred. No. 3.2e-73;
                                                                                                                                                                                                                                                                             Mismatches
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                                                                                                                                                                                                                                                                               38;
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RESULT 10
F84831
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A:Residues: 1-253 <STO>
A:Cross-references: GB:AE002093; NID:g2651297; PIDN:AAB87577.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g40610
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Wature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                probable expansin [imported] - Arabidopsis thaliana
C;Speciles: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: F84831
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C; Superfamily: expansin
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Expansin - upland cotton
C:Species: Gossypium hirsutum (upland
                                                     RESULT 11
T09786
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     123 VAYRRVPCVRRGGIRFTINGHSYENLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN 182
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                                                                                                                                                                                                                                     VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRT-GWQAMSRNWGQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                             169;
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                                                                                                                                                                                                                 VSFRRVPCMKKGGIRFTINGHSYFNLVLISNVGGAGDVHAVSIKGSKTQSWQAMSRNWGQ
                                                                                                                                                                                                                                                                                                NDDPRWCLGSTITVTATNFCPPNPGLSNDNGGWCNPPLQHFDLAEPAFLQIAQYRAGIVP
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                                                                                                                                   NWQSNSYMNDQSLSFQVTTSDGRTLVSNDVAPSNWQFGQTYQG
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75.2%;
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A;Experimental source: cultivar Siokra 1-2 C;Genetics:
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A;Molecule type: mRNA
A;Residues: 1-258 <ORF>
A;Cross-references: EMBL:AF043284; NID:g2811277; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Title: Specific expression of an expansin A; Reference number: 214468; MUID:9655931 A; Accession: T09786
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                                                                                                                                                                                                                                                 A;Gene: At2g39700
A;Map position: 2
C;Superfamily: exp
                                                                                                                                                                                                                                                                                                                                                                                                              A,Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487 A;Accession: D84820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujil, C.Y M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg; S.L.; Fraser, C.M.; Venter Mature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             probable expansin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
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A; Residues: 1-257 <STO>
A; Cross-references: GB:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NNDPQWCISRTITVTATNFCPPNYALSSDNGGWCNPPREHFDLAEPRFLRIAEYRAGIVP
                                        RCQNDGKWCLPG--SIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRA 118
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WQSNAYLNGQSLSFKVTASDGRTITAYNVVPAGWQFGQTFEG
                                                                                 SGGAWQNAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGMSCGACFEL
                                                                                                                                                                   170;
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75.2%;
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                                                                                                                                                                                    75.9%; Score 955; DB 2; Length 257; 73.9%; Pred. No. 1.8e-75;
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Pred. No. 1.3e-76;
6; Mismatches 29
                                                                                                                                                                   Mismatches
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expansin S1 precursor - cucumber
C;Species: Cucumis sativus (cucumber)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 21-Jul-2000
C;Accession: T10079
R;Scherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Shieh, Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995
A;Title: Molecular cloning and sequence analysis of expansins--a highly conserved, multi A;Reference number: Z14894; MUID:96016146
A;Accession: T10079
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-250 <SHC>
A;Cross-references: EMBL:U30382; NID:g1040874; PIDN:AAB37746.1; PID:g1040875
A;Experimental source: cultivar Burpee Pickler
C;Genetics:
A;Gene: EXP1
C;Function:
A;Description: mediates cell wall extension
C;Superfamily: expansin
F;1-23/Domain: signal sequence #status predicted <MAT>
F;24-250/Product: expansin #status predicted <MAT>
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c;Species: Pinus taeda (loblolly pine)
c;Species: Finus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C;Accession: T09825
R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C; Greenwood, M.S.
R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C; Greenwood, M.S.
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C; Superfamily:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Description: Expansins are conserved in A;Reference number: 216866 A;Accession: T09825
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Qy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: mRNA
A; Residues: 1-232 < HUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDB:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       submitted to the EMBL Data Library, July 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Дb
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                                                 Matches 176;
                                                                                           Query Match
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                                                                      Local Similarity
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  GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILYTRVPCLRKGGIRFTVNGHSCFNLVLITNVGGAGDVHAVSIKGPRSGWQPMSRNWGQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMQC
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                                                 Conservative
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    81.5%; sc. 79.3%; Pred. No. ... 79.3%; Pred. No. ...
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                                                               Score 1026; DB 2;
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Pred. No. 7
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'.4e-82;
les 23;
                                                                                      Length 250;
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                                              Indels
                                              0;
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A; Title: Molecular cloning and sequence analysis A; Reference number: Z14894; MUID:96016146 A; Accession: T03298

A; Cross-references: EMBL: U30477;

NID:g1041709;

PIDN:AAB38074.1;

PID:g1041710

A; Molecule type: mRNA A; Residues: 1-251 <SHC>

A; Status: preliminary; translated

from GB/EMBL/DDBJ

C;Species: Oryza sativa (rice)
C;Date: 24-Mar-1999 #sequence\_revision 24-Mar-1999 #text\_change 21-Jul-2000

C; Accession: T03298

R;Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995

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expansins -- a highly conserved,

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R;Cho, H.T.; Kende, H.
Plant Cell 9, 1661-1671, 1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expansin - rice
C;Species: Oryza sativa (rice)
C;Date: 23-Apr.1999 #sequence_revision 23-Apr.1999 #text_change
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T04175
expansin
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C;Superfamily: expansin
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
A; Residues: 1-246 < CHO>
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                        3 GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC
 2 - rice
                                                                                        WQSNAFLDGQSLSFQVTASDGRTVTSNNVAHPGWQFGQTEEG
                                                                                                                          WQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTG
                                                                                                                                                               VSFRRVPCVKKGGIRFTVNGHSYFNLVLVTNVAGAGDVRSVSIKGSRTGWQPMSRNWGQN
                                                                                                                                                                                                                                   DNAGSSCLPGSITVTATNFCPPNYGLPSDDGGWCNPPRPHFDMAEPAFLHIAQYRAGIVP
                                                                                                                                                                                                                                                                   QNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVP 122
                                                                                                                                                                                                                                                                                                        GGWQSAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGAACGSCYELRC
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77.0%;
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Pred. No. 1.7e-79;
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expansin (clone pPtexp3) - loblolly pine (fragment)
C;Species: Pinus taeda (loblolly pine)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
C;Accession: T09821
R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S.
submitted to the EMBL Data Library, July 1996
A;Bescription: Expansins are conserved in conifers and expressed in response A;Reference number: Z16866
A;Accession: T09821
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A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A·Peference number: A84420; MUID:20083487
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C; Superfamily: 6
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C;Genetics:
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A; Residues: 1-248 <STO>
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                                                                                                                                                                                                                                                                                                              Best
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                WOSNSYLNGQSLSFQVTTSDGRTVVSNNVAPSNWQFGQTFEGSQV 232
                                                                                                  VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN 182
                                                                                                                                                                    QNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVP 122
                                                                                                                                                                                                                                        GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          QSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTGAHVR 228
                                                WQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTGAHV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QSNNLLNGQALSFKVTASDGRTVVSNNIAPASWSFGQTFTGRQFR 248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SYRRVPCMRRGGIRFTINCHSYFNLVLVTNVGGAGDVHSVAVKGSRTRWQQMSRNWGQNW 203
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQNW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVPV 123
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                                                                                ILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVHAVSIKGSRSGWQPMSRNWGQN
                                                                                                                                                  NDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIVP 127
                                                                                                                                                                                                                       GGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMRC 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SDGAWCLPGATIVTATNFCPPNNALPNNAGGWCNPPLHHFDLSQPVFQRIAQYKAGVVPV 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GWVNAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIKCQ 83
                                                                                                                                                                                                                                                                                                           Similarity
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                                                                                                                                                                                                                                                                                                       83.2%; Score 1047; DB 2; 79.1%; Pred. No. 1.7e-83;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88.6%; Score 1115; DB 2; 87.1%; Pred. No. 2.3e-89;
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R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library, July 1996
A;Description: Expansins are conserved in conifers and expressed in A;Reference number: Z16866
A;Accession: T09826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expansin (clone pPtexp5) - loblolly pine (fragment)
C:Species: Pinus taeda (loblolly pine)
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 26-May-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: EMBL:U64893; NID:g1778104; PID:g1778105
A;Experimental source: clone pPtexp5
C;Superfamily: expansin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Hutchison, K.W.; Singer, P.B.; Diaz-Sala, C.; Greenwood, M.S. submitted to the EMBL Data Library, July 1996
A;Description: Expansins are conserved in conifers and expressed in response to exoge A;Reference number: 216866
A;Accession: T09818
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-232 <HUT>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C; Accession: T09826
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-232 < HUT>
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Best Local :
                                                                                                                                                                                                                                                                                                                                    Matches 176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 WQSNSYLNGQSLSFQVTTSDGRTIVSNNVAPSNWQFGQTFEGSQV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                183 WQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTGAHV 227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        123 VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  68 NDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLKIAKYRGGIVP
                                                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
ILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVNAVSIKGSRSGWQPMSRNWGQN
                                                                                                                                       QNDGKWCLPGSIVUTATNFCPPNNALPNNAGGWCNPPQQHEDLSQPVFQRIAQYRAGIVP 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIKC
                                                      VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN 182
                                                                                                                                                                                                                                                GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ILYTRVPCLRKGGIRFTVNGHSYFNLVLITNVGGAGDVHAVSIKGSMSGWQPMSRNWGQN 187
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               QNDGKWCLPGSIVUTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVP 122
                                                                                                           NDDPQWCLPGTVTVTATNFCPPNNALPNDNGGWCNPPLQHFDMAEPAFLK IAKYRGG I VP
                                                                                                                                                                                                                      GGWESAHATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNDGLSCGACYEMQC
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                                                                                                                                                                                                                                                                                                                                                        Score 1036; DB 2;
Pred. No. 1.5e-82;
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Pred. No. 4.5e-83;
5; Mismatches 22
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Score
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                                                                                                                                                                                                                                                                                                                                                                                                                  protein search, using sw model
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| 230.5              | 256.5              | 271                | 274                | 274                | 274                | 282                | 287                | 302                | 318.5              | 599                | 662               | 662               | 670                | 780.5             | 784                |
| 18.3               | 20.4               | 21.5               | 21.8               | 21.8               | 21.8               | 22.4               | 22.8               | 24.0               | 25.3               | 47.6               | 52.6              | 52.6              | 53.2               | 62.0              | 62.3               |
| 259                | 491                | 261                | 271                | 259                | 81                 | 276                | 277                | 77                 | 102                | 256                | 257               | 160               | 257                | 255               | 255                |
| 2                  | N                  | 2                  | 2                  | 2                  | N                  | N                  | N                  | 2                  | 2                  | 2                  | Ν                 | N                 | N                  | N                 | N                  |
| E84886             | F96681             | T04301             | H84592             | T50657             | T09830             | T09041             | S48032             | T09815             | T09828             | T05648             | F86259            | T09871            | G96654             | T03299            | T02010             |
| probable beta-expa | protein F1E22.6 (i | beta-expansin - ri | beta-expansin [imp | beta-expansin (imp | expansin (clone pP | cim1 protein homol | cim1 protein - soy | expansin (clone pD | expansin (clone pP | expansin homolog F | protein T12C24.10 | expansin - upland | hypothetical prote | expansin 3 - rice | expansin homolog T |

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 21-Jul-2000 #sequence\_revision 21-Jul-2000 #text\_change 02-Sep-2000
C;Accession: T50654

expansin EXPl [imported] - Arabidopsis thaliana (fragment)

R;Shcherban, T.Y.; Shi, J.; Durachko, D.M.; Guiltinan, M.J.; McQueen-Mason, S.J.; Proc. Natl. Acad. Sci. U.S.A. 92, 9245-9249, 1995

of expansins -- a highly conserved, mu

Shi

A; Molecule type: mRNA A; Residues: 1-237 <SHO

A; Accession: T50654

A; Cross-references: EMBL: U30476; PIDN: AAB38070.

<SHC>

A; Title: Molecular cloning and sequence analysis A; Reference number: Z14894; MUID: 96016146

A; Status: preliminary; translated from GB/EMBL/DDBJ

RESULT 1 T50654

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C; Genetics:
A; Gene: EXP1
C; Function:
probable expansin [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 16-Feb-2001
C;Accession: C844444
                                                                                                                                                                                                                                                                                 A;Description: induces (C;Superfamily: expansin C;Keywords: cell wall
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                                                   RESULT 2
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Best Local
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                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                   induces extension (creep) in plant cell walls
                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                     99.0%;
98.7%;
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                                                                                                                                                                                                                                           Score 1246; DB 2;
Pred. No. 9.4e-101;
1; Mismatches 2;
                                                                                                                                                                                                                                                               Length 237;
                                                                                                                                                                                                                                             Indels
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T07630 T50659 T02727 T50653 T06573 T08016 T10083 T03737 F86335

expansin probable

expansin

expansin S2 precur

R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR000030; PPE.
Fram; PP00169; Pentapeptide_2; 13.
Pfam; PP00823; PPE; 1.
Ilypothetical protein; Transmembrane; Complete proteome.
TRANSMEM 14 POTENTIAL.
TRANSMEM 180 200 POTENTIAL.
TRANSMEM 180 200 POTENTIAL.
CONFLICT 258 258 D -> C (IN REF. 2).
SEQUENCE 678 AA; 66736 MW; 209F1593D52533A2 CRC64;
                                                                         636 FVNAG-----TSISGFFNFGSLMSGFANFDDEVSGYLNGDS 671
                                                                                                              151 ITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQNWQSNSYLNGQS 193
                                                                                                                                                       587 RDEHAEFVTGNSGLANVGNYNAGIINVGDHLSGFRNSVP-----TITGTA--NISG 635
                                                                                                                                                                                                                                                                                                            534 NINTGFFNSGDLNTGLFNSVNQPVQNSG-W-----LHTGTNNSGYANAGTFNSGFDNNA 586
                                                                                                                                                                             99 PQQH--FDLSQPVFQRIAQYRAGIVPV-----AYRR-VPCVRRGGIRFTINGHSYFNLVL 150
                                                                                                                                                                                                                                                           42 ALSTALFNNG-LSCGACFEIR--CQNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNP 98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Wilson R., Ainscough R., Anderson K., Baynes C., Berks M.,
Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson.
Craxton M., Dear S., Du Z., Durbin R., Favello A., Fraser A.,
Fulton L., Gardner A., Green P., Hawkins T., Hillier L., Jier M.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Johnston L., Jones M., Kershaw J., Kirsten J., Laisster N.,
Latreille P., Lightning J., Lloyd C., MortLnore B., O'Callaghan M.,
Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Shownkeen
Sims M., Smaldon N., Smith A., Smith M., Sonnhammer E., Staden R.,
Sulston J., Thierry Meg J., Thomas K., Vaudin M., Vaughan K.,
Watherston D., Thierry Meg J., Thomas K., Vaudin M., Vaughan K.,
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                                                                                 SEQUENCE
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SMART; SM00429; IPT;
SMART; SM00539; NIDO;
SMART; SM00216; VMD;
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01-MAR-2002 (Rel. 41, Last annotation update)
Hypothetical 159.2 kDa protein K03H1.5 in chr
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Rhabditidae; Peloderinae;
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IPR003886; Nidogen_ext.
IPR000436; Sushi_SCR_CCP.
IPR001846; Vwd.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-98295987; PubMed-9634230;
Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F., Badcock K., Basham D., Brown D., Chillingworth T., Connor R., Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L., Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J., Rutter S., Seeger K., Skelton S., Squares S., Squares R., Sulston J.E., Taylor K., Whitehead S., Barrell B.G.; "Deciphering the biology of Mycobacterium tuberculosis from the complete genome sequence.";
Nature 393:537-544(1998).
                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                               iaboratory strains.";
Submitted (APR-2001)
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15-JUL-1999 (Rel. 38, Last sequence upda
16-OCT-2001 (Rel. 40, Last annotation up
Hypothetical PPE-family protein Rv1548c.
RV1548C OR MT1599 OR MTCY48.17.
                                  TubercuList;
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                                                                                                                                                                                                    entities requires a
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MEDITARE-87286864; PubMed=3302672;

Trueheart J., Boeke J.D., Fink G.R.;

"Two genes required for cell fusion during yeast conjugation:
evidence for a pheromone-induced surface protein.";

mol. Cell. Biol. 7:2316-2328(1987).

MOI. Cell. Biol. 7:2316-2328(1987).
                                                                                                                                                                               PMP1_CHLPN STANDARD; PRT; 922 AA. 0929G5; O9K1Y9; O924H9; 16-OCT-2001 (Rel. 40, Created) 16-OCT-2001 (Rel. 40, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation update) 16-OCT-2001 (Rel. 40, Last annotation update)
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PIR; (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entitles requires a license agreement (See http://www.isbor send an email to license@isb-sib.ch).
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                                                                                           Chlamydia pneumoniae (Chlamydophila pneumoniae) Bacteria; Chlamydiales; Chlamydiaceae; Chlamydo
                                                                                                                                                 Probable outer membrane protein pmp1 precursor protein 1) (Outer membrane protein 6).
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 MEDLINE=20007584; PubMed=10539856
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Yeast 7:533-538(1991).
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Read T.D., Brunham R.C., Shen C., Gill S.R., Heldelberg J.F., White O., Hickey E.K., Peterson J., Utterback T., Berry K., Bass Linher K., Weldman J., Khouri H., Craven B., Bowman C., Dodson R. Gwinn M., Nelson W., DeBoy R., Kolonay J., McClarty G., Salzberg Elsen J., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Christiansen G., Boesen T., Hjerno K., Daugaard L., Madsen A.S., Knudsen K., Falk E., Birkelund S.; "Molecular biology of Chlamydia pneumoniae surface prole in immunopathogenicity."; Am. Heart J. 138:S491-S495(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kalman S., Mitchell W., Marathe R., Lammel C., Fan J., Hyman R.W., Olinger L., Grimwood J., Davis R.W., Stephens R.S.; "Comparative genomes of Chlamydia pneumoniae and C. trachomatis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       or send an email to license@isb-sib.ch).
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-!- SIMILARITY: BELONGS TO THE PMP OUTER MEMBRANE PROTEIN FAMILY.
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Gromov P., Madsen P., Gesser B., Tommerup N., Celis J.E.;
"Heterogeneous nuclear ribonucleoproteins H, H', and F are members of
a ubiquitously expressed subfamily of related but distinct proteins
encoded by genes mapping to different chromosomes.";
J. Biol. Chem. 270.28780-28789(1995)
-i- FUNCTION: THIS PROTEIN IS A COMPONENT OF THE HETEROGENOUS NUCLEAR
RIBONUCLEOPROTEIN (HNRNP) COMPLEXES WHILE PROVIDE THE SUBSTRATE
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Belmont J.W., Gibbs R.
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   FOR THE PROCESSING EVENTS THAT PRE-MRNAS UNDERGO
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Pred. No.
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., Ochs H.D.;
n surrounding t
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BECOMING
                                                                                                                                                                                                                                                                                                                                                                                                                                              D.M.,
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01-MAY-1992 (Rel. 2
15-DEC-1998 (Rel. 2
Hypothetical 42.6)
                                                                                                                                                                      YCC8_YEAST P25367;
                                                         Saccharomycetales;
NCBI_TaxID=4932;
                                                                              Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomyc
                                                                                                         YCL028W OR YCL28W OR YCL181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PROSITE; PS00030; RRM_RNP_1; Nuclear protein; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U01923; -; NOT_ANNOTATED_CDS. EMBL; U78027; AAB64202.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTIONAL, TRANSLATABLE MRNAS IN THE CYTOPLASM. BINDS POLY (RG)
-:- SUBCELLULAR LOCATION: Nuclear; nucleoplasm.
-:- TISSUE SPECIFICITY: EXPRESSED UBIQUITOUSLY.
-:- SIMILARITY: CONTAINS 3 RNA RECOGNITION MOTIFS (RRM).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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                                                                                                                                                                                                                                                                                             EADVEFATHEDAVAAMAKDKANMQHRYVELFLNSTAGTSGGAYDHSYVELFLNSTAGASG
                                                                                                                                                                                                                                                                                                                                            GMSDHRYGDGGSSFQSTTGHCVHMRGLPYRATENDIYNFFSPLNPMRVHIEIGPDGRVTG
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                                                                                                                                                                                                                                                                                                                                                                                                                  GGGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIR 61
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RNA-BINDING (RRM)
RNA-BINDING (RRM)
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SEQUENCE FROM N.A.
MEDLINE-91377317; PubMed-1897318;
Rad M.R., Luetzenkirchen K., Xu G.,
"The complete sequence of a 11,953 ]

dq

Kleinhans U., Hop fragment from

Hollenberg C....

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RESULT 9
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                                                                                                                                                                                                                                                                                                                                                                                          PERIOD. ENGL. 14:741-73 (1597).

TOROL. BIGL. EVOL. 14:741-73 (1597).

FUNCTION: ESSENTIAL FOR BIOLOGICAL CLOCK FUNCTIONS. DETERMINES THE PERIOD LENGTH OF CIRCADIAN AND ULTRADIAN RHYTHMS; AN INCREASE IN PER DOSAGE LEADS TO SHORTENED CIRCADIAN RHYTHMS AND A DECREASE LEADS TO LENGTHENED CIRCADIAN RHYTHMS AND A DECREASE LEADS TO LENGTHENED CIRCADIAN RHYTHMS AND A DECREASE RHYTHMIC COMPONENT OF THE MALE COURTSHIP SONG THAT ORIGINATES IN THE THORACIC NERVOUS SYSTEM. THE BIOLOGICAL CYCLE DEPENDS ON THE RHYTHMIC FORMATION AND NUCLEAR LOCALIZATION OF THE TIM-PER COMPONENT OF PER. NUCLEAR ACTIVITY OF THE HETERODIMER COMPLEX. LIGHT INDUCES THE DEGRADATION OF THE TRANSCHIPTION THROUGH A NEGATIVE FEEDBACK LOOP. BEHAVES AS A NEGATIVE ELEMENT IN CIRCADIAN TRANSCRIPTIONAL LOOP. DECS NOT APPEAR TO BIND DNA, SUGGESTING INDIRECT TRANSCRIPTIONAL HIBSTION (BY SHILARITY).

11- SUBUNIT: FORMS HETERODIMER WITH TIMELESS (TIM); THE COMPLEX THEN TRANSCLOCATES INTO THE NUCLEUS (BY SIMILARITY).

11- SUBCELLULAR LOCATION: NUCLEAR AT SPECIFIC PERIODS OF THE DAY. FIRST ACCUMULATES IN THE PERINUCLEAR REGION ABOUT ONE HOUR BEFORE FOR NUCLEAR LOCALIZATION (BY SIMILARITY).

11- PTM: PHOSPHORYLLATED WITH A CIRCADIAN RHYTHMICITY, PROBABLY BY THE DOUBLE-TIME PROTEIN (DBT). PHOSPHORYLLATED IN THE STABILITY OF PER MONOMER AND IN THE FORMATION OF HETERODIMER DEPARTMENT OF PER MONOMER AND IN THE FORMATION OF HETERODIMER DEPARTMENT OF PER MONOMER AND IN THE FORMATION OF HETERODIMER DEPARTMENT.
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15-JUL-1999
                                                                                                                                                                                                                                                              the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PER_DRONE
P91686;
                                                                                                                                                                                                                                                                                                                                              This
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Interspecific and intraspecific comparisons of the period locus the Drosophila willistoni sibling species."; Mol. Biol. Evol. 14:741-753(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila nebulosa (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
                                                                                                                                                    Biological
                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-0761.0 PALMIRA / COLOMBIA;
MEDLINE-97357421; PubMed-9214747;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ephydroidea; Dro
NCBI_TaxID=7271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pterygota; Neoptera; Endopterygota;
  SEQUENCE
                                                                                                                                                                        FlyBase;
                                                                                                                                                                                          EMBL; U51090; AAB41386.1; -
                                                                                                                                                                                                                                                entities requires a
                                                                                                                                                                                                                                                                                                                            between
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gleason J.M., Powell J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PER
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                                                                                                                                                                                                                                                                                  SWISS-PROT entry is copyright. It is produced through a collaboration een the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                  PER-TIM (BY SIMILARITY).
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                                                                                                                                                                      FBgn0018750;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (Rel. 38, Created)
(Rel. 38, Last sequence update)
(Rel. 38, Last annotation update)
                                                                                                                                                    rhythms;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophilidae; Drosophila
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein (Fragment)
                                                                                                                                                                                                                                                license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                      Repeat;
  39104
                                                                                                                                                                    Dneb\per.
  W.
                                                                                                                                                      Nuclear protein; Phosphorylation
                                                      POLY-GLY.
                                                                                            POLY-GLY.
POLY-SER.
  A6C519E2CE66D5F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Diptera;
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                                                                                                                                                                                                                                                                    Usage
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Best Local S
Matches 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sol-Church K., Frenck J., Troeber D., Mason R.W.;
"Cloning of a mouse cysteine protease.";
Submitted (JUN-1999) to the EMBL/GenBank/DDBJ databases
-:- SUBCELLULAR LOCATION: Lysosomal (Potential).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-Embryo;
MEDLINE-99456833; PubMed-10526153;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9R014; Q9WV51;
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
16-OCT-2001 (Rel. 40,
                                                                           PROSITE; PS00139; THIOL_PROTEASE_CYS; PROSITE; PS00639; THIOL_PROTEASE_HIS; PROSITE; PS00640; THIOL_PROTEASE_ASN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tisljar K., Deussing J., Peters C.; "Cathepsin J, a novel murine cysteine with a placenta-restricted expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Chordata; Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                      MGD; MGI:1349426; Ctsj.
InterPro; IPR000668; Peptidase_C1.
InterPro; IPR000169; Thiolprot_act_site.
                                                                                                                                                                                                                                                                                                                                                                        EMBL; AF136272; AAF13142.1; -. EMBL; AF158182; AAD41898.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -1- TISSUE SPECIFICITY: EXPRESSED IN PLACENTA.
-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1; ALSO KNOWN AS THE PAPAIN FAMILY OF THIOL PROTEASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEBS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CTSJ OR CTSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cathepsin
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                                                         Hydrolase;
                                                                                                                                                                         PRINTS; PR00705; PAPAIN.
                                                                                                                                                                                              Pfam; PF00112; Peptidase_C1; 1.
                                                                                                                                                                                                                                                                                                                       MEROPS; C01.038;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           entities requires a license agreement
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=C57BL/6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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PROPER
                                                                                                                                                                                                                                                                                                                                                   HSSP;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGG-----GGGGGAGSASGTCGTGNNGAGGGGGSNAQSSTNQYTQSGLSC----
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                                                                                                                                                                                                                                                                                                                                                P07711;
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                                                   Thiol protease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     precursor
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18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE-Placenta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7.5%;
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Last annotation update)
(EC 3.4.22.-) (Cathepsin P) (Catlrp-p)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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                                                   Glycoprotein; Lysosome;
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Pred. No. 0.52;
   ACTIVATION PEPTIDE
                              POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Craniata; Vertebrata; Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
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                                                         Zymogen; Signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed. entities requires a license agreement (See )
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01-FEB-1995 (Rel. 31, Last sequenc
01-MAR-2002 (Rel. 41, Last annotat
Pollen allergen Zea m 1 (Zea m I).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Allergen; Multigene family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MaizeDB; 65840;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gene 131:227-230(1993).
-!- TISSUE SPECIFICITY: POLLEN TISSUE.
-!- DEVELOPMENTAL STAGE: EXPRESSION LOW BEFORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bedinger P.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Spermatophyta; Magnoliophyta; Panicoideae; Andropogoneae; Zo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MPZ1_MAIZE
Q07154;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DOMAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; L14271; AAA33496.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             rye grass.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Broadwater A.H., Rubinstein A.L., Chay C.H., Klapper D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=94010312; PubMed=8406014;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TISSUE=Pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=4577;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Zea mays (Maize).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Zea mI, the maize homolog of the allergen-encoding Lol pI gene
                                                                                                                                                                                    47
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SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS
QTIVSNNXANAGWSFGQTFT::::: | | :|
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       POLLEN MITOSIS.
                                                                              VAVLVKFVADDGDIVLMEIQDKLSAEWKPMKLSWGAIWRMDTAKALKG-PFSIRLTSESG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 JC1524; JC1524.
                                                                                                                                                                                                                                                                                          TACGNVPIFKDGKGCGSCYEVRCKEKPE-CSGNPVTVFITDMNYEP---
                                                                                                                                                                                                                                                                                                                                        TAALSTALFUNGLSCGACFEIRCQNDGKWCL--PGSIVVTATUFCPPUNALPUNAGGWCN
                                                                                                                           -LVLITNVGGAGDVHSAMVKGSRTG-WQAMSRNWGQNWQSNS--YLNGQSLSFKVTTSDG
                                                                                                                                                                                                                                  PPQQHFDLSQPVFQRIAQ----YRAGIVPVAYRRVPCVRRGGIRFTINGHSYFN---
                                                                                                                                                                                 IAPYHFDLSGKAFGSLAKPGLNDKLRHCGIMDVEFRRVRCKYPAGQKIVFHIEKGCNPNY
                                                                                                                                                                                                                                                                                                                                                                                                49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          s requires a license agreement (See http://www.isb-sib.ch/announce/
an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PR01225; EXPANSNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 105
191 AA;
                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 91
186
-- 21362 MW;
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24.5%;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                              37;
                                                                                                                                                                                                                                                                                                                                                                                                                      Score 166;
Pred. No. 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
; 6E2A9DF921C45C63 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Liliopsida; Poales; Poaceae; PACC clade;
                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    191
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1es 82;
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51 13 4

----GLSCGACFEIR-----GAVSAYKATTTRYYDGQE---

-CQNDGKWCLPG-SIVVTATNFCPPNNALPNNAGGWCNPP

99 66 50

-GACGCGSSSGAFPWQLGIGNGVYTAAGSQALFDTAG

----GYGTNTAALSTALFNN--

29

GWVNAH - - - - ATFYGGGDASGTMGGACGYGNLYSQ - - -

Matches Query Match Best Local :

42;

Conservative

12; Score Pred.

Mismatches 110.5; No. 0.0

35; ۲.

Indels Length

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10;

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Similarity

8.8%; 24411 MW;

CARBOHYD DISULFID DISULFID

SEQUENCE

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242 27 134 182 205 242 182 230

PRO/SER-RICH (LINKER).
CELLULOSE-BINDING (BY SIMILARITY).
N-LINKED (GLCNAC. . .) (POTENTIAL)

.) (POTENTIAL)

BY SIMILARITY.
BY SIMILARITY.

CC033FC51326C71D CRC64;

ENDOGLUCANASE V.
NUCLEOPHILE (BY SIMILARITY).
PROTON DONOR (BY SIMILARITY).
CATALYTIC.

CHAIN ACT\_SITE ACT\_SITE

PROSITE; PS50842; EXPANSIBLE PROSITE; PS01140; GLYCOSYL\_HYDROL\_F45; 1.

PROSITE; PS00562;

PS00562; CBD\_FUNGAL; 1. PS50842; EXPANSIN\_EG45; 1.

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RESULT 8
GUN5_TRIRE
                                                                                                                                                                                                                              InterPro; IPR000334; Glyco_hydro_45.

Pfam; PF00734; CBD_1; 1.

Pfam; PF02015; Glyco_hydro_45; 1.

Pr0Dom; PD001821; CBD_fungal; 1.

SMART; SM00236; fCBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
Endoglucanase V precursor (EC 3.2.1.4) (Endo-1,4-beta-glucanase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GUN5_TRIRE
P43317;
                                                                                                                                                                                                                                                                                                                                                                                This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                          EMBL; 233381; CAA83846.1; HSSP; P00725; 2CBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Saloheimo A., Henrissat B., Hoffren 
"A novel, small endoglucanase gene, 
isolated by expression in yeast."; 
Mol. Microbiol. 13:219-228(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN=QM9414 / RUT C-30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Trichoderma reesei (Hypocrea jecorina).
Eukaryota; Fungi; Ascomycota; Pezizomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EGL5
                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       linkages in cellulose.
-!- SIMILARITY: BELONGS TO CELLULASE FAMILY K (FAMILY 45 OF GLYCOSYL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=95075308; PubMed=7984103;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypocreales; Hypo
NCBI_TaxID=51453;
                                                                                                                                                                                                                                                                                                        InterPro; IPR000254; CBD_fungal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HYDROLASES).
SIMILARITY: CONTAINS 1 FUNGAL-TYPE CELLULOSE-BINDING DOMAIN (CBD).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   . Microbiol. 13:219-228(1994).
CATALYTIC ACTIVITY: Endohydrolysis of 1,4-beta-D-glucosidic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypocreaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypocrea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A.-M., Teleman O., Penttilae M.; egl5, from Trichoderma reesei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 242 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sordariomycetes;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -I- SUBCELLULAR LOCATION: Secreted.
-I- DISEASE: CAUSES GRASS POLLEN ALLERGY.
-I- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS
-I- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-I- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Suphioglu C., Singh M.B., Simpson R.J., Ward L., Knox R.B.; "Identification of canary grass (Phalaris aquatica) pollen allergens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                pollen.";
Clin. Exp. Allergy 25:853-865(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-96105569; PubMed-8564724; Suphioglu C., Singh M.B.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Phalaris aquatica (Canary grass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldea
                                                                                                                                                                                                                                                                                                                                                   CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   by immunoblotting: IgE and IgG antibody-binding Allergy 48:273-281(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning, sequencing and expression in Escherichia coli of Pha a and four isoforms of Pha a 5, the major allergens of canary grass
                                                                                                                                                                                                                                                                                                                                                                                                                                 Allergen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-93319091; PubMed-7687099;
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                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                     CONFLICT
                                                                                                                                                                                                                                                                                                                                                                     DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                              PROSITE; PS50842; EXPANSIN_EG45; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS;
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                                                                                                                          104
 211
                               168
                                                             151
                                                                                                                                                        60
                                                                                                                                                                                        44
 GKDKWIELKESWGAIWRIDTPDKLTG-PFTVRYTTEGGTKAEFEDVIPEGW 260
                                                                                                                          LKCSKP-ESCSGEPITVHITD----DNEEP-----IAPYHFDLSGHAFGSMAKKGEE
                                                                                                                                                                                        GDKWLDAKSTWYGKPTGAGPKDNGGACGYKDVDKAPFNGMTGCGNTPIFKDGRGCGSCFE
                                                                                                                                                                                                                      GGGWVNAHATFYGGGDASGTM--GGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFE
                            SRTGWQAMSRNWGQNWQSNS--YLNGQSLSFKVTTSDGQTIVSNNXANAGW
                                                             ENVRGAGELELQFRRVKCKYPDGTKPTFHVEKGSNPNYLALLVKYVDGDGDVVAVDIKEK
                                                                                         ---YRAGIVPVAYRRVPCVRRGGIRETIN----GHSYFNLVLITNVGGAGDVHSAMVK-G
                                                                                                                                                        IRCQNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQ----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF01357; Pollen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P43214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            S80654; AAB35984.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PD002179;
                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PR01225; EXPANSNEAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PD002179; Pollen_allergen; 1. PS50843; EXPANSIN_CBD; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Glycoprotein; Signal.
                                                                                                                                                                                                                                                                                                                     269 AA;
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EXPANSIN-LIKE EG45.
EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC. . .) (POTENTIAL).
P -> G (IN REF. 2).
                                                                                                                                                                                                                                                                    Score 199; DB 1;
Pred. No. 4.8e-10;
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Best Local
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CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      -:- TISSUE SPECIFICITY: EXPRESSED IN MATURE VEGETATIVE OR OTHER FLORAL TISSUES.
-!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning, expression and immunological characterization of Ory s the major allergen of rice pollen."; Gene 164:255-259(1995).
-I- SUBCELLULAR LOCATION: Secreted.
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PROSITE; PS50842;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
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                               TKITFHIEKASNPNYLALLVKYVAGDGDVVEVEIKEKGSEE-WKALKESWGAIWRIDTPK
                                                          IRFTIN----GHSYFNLVLITNVGGAGDVHSAMV--KGSRTGWQAMSRNWGQNWQSNS--
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otein; Signal; Multigene family.
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29.5%;
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Pred. No. 1.0
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EXPANSIN-LIKE CBD.
N-LINKED (GLCNAC. . .) (PC)
B1C5F24EA398DD60 CRC64;
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MAJOR POLLEN ALLERGEN
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01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Major pollen allergen Hol 1 1 precursor (Hol 1 I) (Hol 1 1.0101 and
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STRAIN=CV. Bufe A., Becker W.M.,
                                                                                                                                                                                                                                                                                                             Spermatophyta; Magnoliophyta; Poeae; Holcus.
                                                                                                                                                                                                                                                                                                                                                                              Holcus lanatus (Velvet grass).
Eukaryota; Viridiplantae; Stre
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ProDom; PD002179; Pollen_allergen;
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                                                                         Submitted (NOV-1993) to the
                                                                                                                                                                                         SEQUENCE FROM N.A.
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Pred. No. 5.5e-11;
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                                                                                                                                                                                                                                                                                                                                        Embryophyta; Tracheophyta;
a; Poales; Poaceae; Pooidea
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DOMAIN
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J. Allergy Clin. Immunol. 99:781-787(1997).
[3]
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PROSITE; PS50843; EXPANSIN_CBD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNFAMLY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. The use by non-profit institutions as long modified and this statement is not removed
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                                                                                                                                                             SRTGWQAMSRNWGQNWQSNS--YLNGQSLSFKVTTSDGQTIVSNNXANAGW
                                                                                                                                                                                                                 QKLRSAGELELKFRRVKCKYPDGTKPTFHVEKGSNPNYLALLVKYIDGDGDVVAVDIKEK
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Pred. No. 4.7e-10;
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T -> S (IN HOL L 1
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                                                                                                                                                                                                                                                                                                                      -----IAPYHFDLSGHAFGSMAKKGEE 146
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01-APR-1990 (Rel. 14, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pollen allergen Lol p 1 precursor (Lol p I) (Allergen
                                                                                        I allergenic determinant.",

MO1. Immunol. 26:557-561(1989).

-!- SUBCELLULAR LOCATION: Secreted.
-!- DISEASE: CAUSES GRASS POLLEN ALLERGY.
-!- SIMILARITY: BELONGS TO THE LOL P I FAMILY OF ALLERGENS.
-!- SIMILARITY: BOUNTAINS 1 EXPANSIN-LIKE EG45 DOMAIN.
-!- SIMILARITY: CONTAINS 1 EXPANSIN-LIKE CBD DOMAIN.
           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                   proteins from rye-grass (Lolium perenne) pollen prepared by a and efficient purification method.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-91160716; PubMed-2001733; Griffith I.J., Smith P.M., Pollock J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poeae; Lollum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Lollum perenne (Perennial ryegrass).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
modified
                                                                                                                                                                                                                     Esch R.E., Klapper D.G
                                                                                                                                                                                                                                      MEDLINE-89364850; PubMed-2475768;
                                                                                                                                                                                                                                                     SEQUENCE OF 236-263
                                                                                                                                                                                                                                                                                                                                                    Cottam G
                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-86242068; PubMed-3718469;
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Pollen,
                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                               rye-grass pollen.";
FEBS Lett. 279:210-215(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Pollen;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           allergen Lol p I."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Perez M., Ishioka G.Y., Walker L.E., Chesnut R.W "cDNA cloning and immunological characterization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. MEDLINE-90375479; PubMed-1697854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOLPR
                                                                                                                                                                                                                                                                                                                                   "Physicochemical and immunochemical characterization of allergenic
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A., Davies S., Hough T., Singh M.B., Simpson R.J.
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removed.
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commercia
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Best Local
                                                                                           PHLPI.
Phleum pratense (Common timothy).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Liliopsida; Poales; Poaceae; Pooidea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
CONFLICT
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VARIANT
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                      Laffer S., Valenta R., V
Scheiner O., Duchene M.;
                                                                                                                                                01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
Pollen allergen Phl p 1 precursor (Phl p I)
                                                                                                                                                                                                     MPP1_PHLPR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                           MEDLINE=95015525; PubMed=7930302;
                                                       TISSUE-Pollen;
                                                                SEQUENCE FROM N.A.
                                                                                   NCBI_TaxID=15957;
                                                                                                                                                                                          P43213;
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            "Complementary
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  (Phleum
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pS50843;
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EXPANSIN_CBD; 1.
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Copyright (c) 1993 - 2002 Compugen Ltd.
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ROH2_HUMAN
YCC8_YEAST
PMP1_CHLPN
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MPL1_LOLLPR
MPP1_PHLPR
MPP1_HOLLA
MPA1_PHAAQ
MPO1_ORYSA
MPC1_MAIZE
GUN5_TRIRE
PER_DRONE
EGG2_SCHJA
LI112_CAEEL
YV77_SYNY3
VG37_BPT2
OWBB_RICJA
PORD_PSEAE
PORD_PSEAE
VG32_BPMD2
SB87_DICDI
YGN1_YEAST
Y462_TREPA
L120K_RICRI
OMPB_RICRI
OMPB_RICRI
SECG_HAEIN
RCH1_HUMAN
GRP2_PHAVU
VP4_ROTGI
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P14946 lolium pere
P43213 phleum prat
P43216 holcus lana
Q41260 phalaris aq
Q40638 oryza sativ
Q07154 zea mays (m
P43317 trichoderma
P91686 drosophila
P917014 mus musculu
P55795 homo sapien
P25367
P34501
P34501
P321869
P1921869
P134585
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| Query Maest Lou                    | EMI HSS Int Pfc PR: PRC PRC PRC CALL CALL EMI                                                                                     | This betwe the E use modif entit or se                                                                                                                                                                                                                                                                                                                                   |                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | SEC<br>Smt                                                 | 16<br>01<br>Mai<br>CYN<br>CYN<br>Eul<br>Spe<br>Chl                | SULT 1<br>CYN<br>MPC<br>MPC<br>OO4 | 35<br>35<br>35<br>37<br>38<br>39<br>44<br>44<br>44<br>44<br>44<br>44<br>44<br>44<br>44<br>44<br>44<br>44<br>44                              |
| / Match<br>Local Simi<br>res 62;   | P; P432<br>m; P601<br>MYS; PR<br>DOM; PD<br>DOM; PD<br>SSITE; P<br>SSITE; P<br>ergen.<br>AIN<br>AIN<br>AIN                        | This SWISS-P between the the European use by non modified and entities req or send an e                                                                                                                                                                                                                                                                                  | "Cloning and expression in active form of Cyn d 1, the J. Allergy Clin. Immunol. 9: 1- SUBCELLULAR LOCATION: S. 1- DISEASE: CAUSES GRASS P. 1- SIMILARITY: BELLONGS TO: 1- SIMILARITY: CONTAINS 1: SIMILARITY: CONTAINS 1: SIMILARITY: CONTAINS 1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | PUENCE FROM SSUE=POllen; SLINE=963479 Lth P.M., Suhh M.R.; | po<br>po<br>po<br>po<br>po<br>po<br>po<br>po                      | 1<br>YNDA<br>MPC1_CYNDA            | 78.5<br>78.5<br>78.5<br>78.5<br>78.7<br>78.7<br>78.7<br>78.7                                                                                |
| nilarity<br>Conserv                | 3; AAB5(<br>4; 1WHO)<br>1PR000888<br>157; Polli<br>1225; E3<br>102179; I<br>150843; I<br>150842; I<br>159<br>159<br>246 AA;       | SWISS-PROT entry is copyright. It is produced wen the Swiss Institute of Bioinformatics and juropean Bioinformatics Institute. There are not by non-profit institutions as long as its colled and this statement is not removed. Usage lied and this statement is not removed. Usage ites requires a license agreement (See http://wind an email to license@isb-sib.ch). | n of Cyn<br>Clin. In<br>JULAR LOC<br>S: CAUSES<br>RITY: BEI<br>RITY: CON                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | OM N.A.,<br>en;<br>47957; p<br>suphiog                     | 10 x x x x x x 0 x x x x                                          | S                                  | $\begin{array}{cccccccccccccccccccccccccccccccccccc$                                                                                        |
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Hutchison K.M., Singer P.B., Diaz-Sala C., Greenwood M.S.;
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exogenous auxin.";
Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
EMBL; U64890; AAB40634.1;
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InterPro; IPR000882; Pollen_allergen.
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                                                                                                                                                                                                                                                                            MEDLINE-99329318; PubMed=10398718; Hutchison K.W., Singer P.B., McInnis S., "Expansins are conserved in conifers and response to exogenous auxin."; Plant Physiol. 120:827-832(1999).
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PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen;
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    3 GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC
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Ida; Coniferales; Pinaceae;
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lda; Coniferales; Pinaceae;
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                                              Score 1047; DB 10;
Pred. No. 2e-87;
6; Mismatches 21;
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           P93492 PRELIMINARY;
P93492;
01-MAY-1997 (TrEMBLrel. 03, C
01-MAY-1997 (TrEMBLrel. 03, I
01-DEC-2001 (TrEMBLrel. 19, I
EXPANSIN (FRAGMENT)
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                      InterPro; IPR000882; Pollen_allergen.
Pfam; Pf01357; Pollen_allergen; 1.
PRINTS; PR01225; ExPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
SEQUENCE 245 AA; 26201 MW; F66E26114C27E360 CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                               Im K.H., Cosgrove D.J., Jones A.M.;
"Subcellular localization of expansin plant physiol. 123:463-470(2000).
EMBL; AF230332; AAF35901.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDLINE-20317189; PubMed-10859177;
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(Loblolly pine).
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ProDom; PD002179; Pollen_allergen;
SEQUENCE 242 AA; 26157 MW; 168/
                                                                                                                                                                                                 Im K.H., Cosgrove D.J., Jones A.M.;
"Subcellular localization of expansin
Plant Physiol. 123:463-470(2000).
EMBL; AF230333; AAF35902.1;
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                                                                                                                                                  Pfam; PF01357; Pollen_allergen; 1.
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Eukaryota; Viridiplantae;
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01-OCT-2000
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01-DEC-2001 (TrEMBLrel.
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MEDLINE=20317189; PubMed=10859177;
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                                                                                                                                                                              InterPro; IPR000882; Pollen_allergen
                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=34245;
                                                                                                                                                                                                                                                                                                                                                                                      Heliantheae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           123 VAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTGAHVR 228
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Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                    Zinnia
                  83.5%;
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19,
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Last annotation update)
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Last annotation update)
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                  Score 1051.5;
Pred. No. 7.5e
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4; Mismatches
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Pred. No. 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
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                                                                                        168A01724FCF5B58 CRC64;
Mismatches
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                         .5e-88;
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Best Local :
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P93493;
01-MAY-1997
01-MAY-1997
01-DEC-2001
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01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-DEC-2001 (TrEMBLrel. 19,
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PRINTS; PRO1225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
ProDom; PD002179; Pollen_allergen; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  during Tomato Seed Germination.";
Plant Physiol. 124:1265-1274(2000).
EMBL; AF18423; AAG329211; .
InterPro; IPR000882; Pollen_allergen.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;

Asteridae; euasterids I; Solanales; Solanaceae; Solanum.
                                                                                                        P93493
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                                                                                                                                                                                                                                         QSNALLDGQILSFKYTTGDGRTVFCNNAIPAGWSFGKTYTGA
                                                                                                                                                                                                                                                                                             QSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTGA
                                                                                                                                                                                                                                                                                                                                                                          AYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQNW 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                          GDSKWCLPGSIVVTATNFCPPNFALPNNAGGWCNPPLHHFDLAQPVFQKMAQYRAGIVPV 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIVPV 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GWIEAHATFYGGGDASGTMGGACGYGNLYSEGYGTNTAALSTALFNNGLSCGSCFELKCV 85
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Interpro; IpR0000882; Pollen_allergen.
Pfam; PF01357; Pollen_allergen; 1.
PF1NTS; PR01225; EXPANSNFAMLY.
PRODOM; PD002179; Pollen_allergen; 1.
SEQUENCE 248 AA; 26482 MW; 29E3199269B71271 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-ROOTS TREATED WITH DMBQ;
MEDLING-21186069; Pubmed-11290422;
Wrobel R.L., Yoder J.L.;
"DifferentLal RNA expression of alpha-expansin gene family members in the parasitic angiosperm Triphysaria versicolor (Scrophulariaceae).";
Gene 266.85-93(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Triphysaria versicolor.
Eukaryota; Viridiplantae; Streptopl
Spermatophyta; Magnoliophyta; eudic
Asteridae; euasterids I; Lamiales;
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PRINTS; PR01225; EXEANSNEAMLY.
Probom; P0002179; P0011en_allergen; 1.
SEQUENCE 249 AA; 26116 MW; DC976FEE376794FF CRC64;
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3 GGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIRC
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                                                                                                                Conservative
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87.5%;
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87.1%;
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                                                                                                                    17;
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Last annotation update)
                                                                                                                                                Score 1106.5; DB 10; Pred. No. 7.7e-93;
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Q1-MAY-1999 (TrEMBLrel. 10,
Q1-MAY-1999 (TrEMBLrel. 10,
Q1-DEC-2001 (TrEMBLrel. 19,
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                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF01357; Pollen_allergen; 1. PRINTS; PR01225; EXPANSNFAMLY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Acid-growth response and alpha-expansins in bright yellow 2 tobacco."; plant Physiol. 118:907-916(1998). EMBL; AF049353; AAC96080.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=99026292; PubMed=9808735;
Link B.M., Cosgrove D.J.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nicotiana tabacum (Common tobacco)
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                                                                                                                                                                                            CQNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV 121
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                                                                                                                NWQSNSYLNGQSLSFKVTTSDGQTIVSNNXANAGWSFGQTFTGA 225
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                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                 21
249 AA;
                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                            86.7%;
85.3%;
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                                                                                                                                                                                                                                                                                                            Score 1092; DB 10;
Pred. No. 1.6e-91;
                                                                                                                                                                                                                                                                                                                                                            ALPHA-EXPANSIN
                                                                                                                                                                                                                                                                                                                                                                            POTENTIAL.
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Best Local
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01-MAR-2001
01-DEC-2001
EXPANSIN 2.
                                                                                                                                                      InterPro; IPR000882; Pollen_allergen.
PRINTS; PR01225; EXPANSNFAMLY.
ProDom; PD002179; Pollen_allergen; 1.
SEQUENCE 249 AA; 26428 MW; 63D014
                                                                                                                                                                                                                                    SEQUENCE FROM N.A. Wu Z., Wiersma P.A.;
                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta; eurosids I; Rosales; Rosaceae;
                                                                                                                                                                                                                                                                                                   Prunus avium (Cherry).
Eukaryota; Viridiplantae;
                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                    NCBI_TaxID=42229;
                                                                                                                                                                                                                                                                                                                             EXP2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (JAN-2000) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  abscission zone.";
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 86
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les 202; Conserv
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           CQNDGKWCLPGSIVVTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV 121
 CVNDPKWCLPGAIVVTATNFCPPNNALPNNAGGWCNPPQHHFDLSQPVFQHIAQYKAGVV
                                                       GGGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVSYRRVPCRRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAAIKGSRTVWQAMSRNWGQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWGQ 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CENDGKWCLPGSIVVTATNFCPPNNALANNNGGWCNPPLEHFDLAQPVFQRIAQYRAGIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CQNDGKWCLPGSIVYTATNFCPPNNALPNNAGGWCNPPQQHFDLSQPVFQRIAQYRAGIV 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GGGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEIR
                                             GGGWVDARATFYGGSDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLGCGSCYEIR
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AF229437; AAF61712.1;
AF229431; AAF61713.1;
                                                                                        202;
                                                                                                  Similarity
                                                                                                                                             PD002179; Pollen_allergen;
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                                                                                                                                  252 AA;
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                                                                                        Conservative
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                                                                                              90.3%;
89.0%;
                                                                                                                                    26766 MW;
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89.0%;
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                                                                                                                                                                                                                                                                             Streptophyta; Embryophyta; Tracheophyta; yta; eudicotyledons; core eudicots; Rosid ceae; Amygdaloideae; Prunus.
                                                                                        11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12;
                                                                                                                                                                                                                                                                                                                                               Created)
Last sequence update)
Last annotation update)
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Pred. No. 8.
                                                                                                   Score 1137;
Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                  5C62EBF83E5A138E CRC64;
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                                                                                                 .3e-95;
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Prunus.
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RESULT 6
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AC 0806
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DT 01-C
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OX NCB1
RN I11
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RX MEDI
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Best Local S
Matches 196
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01-DEC-2001
01-DEC-2001
01-DEC-2001
STRAIN-CV. COLUMBIA;
MEDLINE-20083487; PubMed=10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P.,
Fujii C.Y., Mason T.M., Bowman C.L., Barnst
Buell C.R., Ketchum K.A., Lee J.J., Ronning
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-FRUIT ABSCISSION ZONE;
YOO S.-D., van Nocker S.;
Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases
EMBL; AF350938; AAK48847.1; .
SEQUENCE 249 AA; 26397 MW; C65556B03BAB99D0 CRC64;
                                                                                                                    AT2G03090.
Arabidopsis thaliana (Mouse-ear cress).
Brassidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosideurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                            01-NOV-1998 (TremBLrel.
01-NOV-1998 (TremBLrel.
01-DEC-2001 (TremBLrel.
PUTATIVE EXPANSIN.
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Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
eurosids I; Rosales; Rosaceae; Amygdaloideae;
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                                                                           SEQUENCE FROM N.A
                                                                                                      NCBI_TaxID=3702
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                                                                                                                                                                                                                                                                                                                                                                                                         VPVSYRRVPCIKKGGVRFTINGHSYFNLVLITNVGGAGDVHAVSIKGSKTGWQTMSRNWG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RCASDPKWWLPGSIFVTATNFCPPNNAPPNNAGGWCNPPQQHFDLAQPVFQRIAQYRAGI 142
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! (TrEMBLrel.
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87.5%;
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19,
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Pred. No. 4
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   Ronning
 T.P., Benito M.-I., Town C.D.,
Barnstead M.E., Feldblyum T.V.
Ronning C.M., Koo H., Moffat K.
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                                                                                               Query Match
Best Local :
                                                                    Matches
                                                                                                                                                                                                                                                          Nature 408.816-820(2000).
EMBL; AF360291; AAK26001.1; -.
EMBL; AC073178; AAG60095.1; -.
InterPro; IPR000882; Pollen_allergen.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K., Goldsmith A.D., Lee J.M., Quach H.L., Toriumi M., Yu G., Bowser I Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones Kamilya A., Karlin-Neumann G., Kawai J., Kim C., Lam B., Lin J., Miranda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana (Mouse-ear cress).

Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F10D13_18
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01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE EXPANSIN PROTEIN (AT-EXP1).
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Q9C554;
                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (MAR-2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MLEdnda M., Narusaka M., Nguyen M., Palm C.J., Sakurai T., Satou M.,
Seki M., Shinn P., Southwick A., Shinozaki K., Davis R.W., Ecker J.R.,
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  1 AGGGWVNAHATFYGGGDASGTMGGACGYGNLYSOGYGTNTAALSTALFNNGLSCGACFEI 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VPVAYRRVPCVRRGGIRFTINGHSYFNLVLITNVGGAGDVHSAMVKGSRTGWQAMSRNWG
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                                                                                               Similarity
                                                                                                                                                                            PR01225; EXPANSNFAMLY
PD002179; Pollen_allergen;
E 250 AA; 26518 MW; 1D9;
                                                                 Conservative
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                                                                                      99.0%;
98.7%;
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                                                                                      Score 1246;
Pred. No. 1
                                                                                                                                                                         1D95EBA24FCFE7E5 CRC64;
                                                              Mismatches
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                                                                                      .6e-105;
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                                                                                                                    DB 10;
                                                           Indels
                                                                                                                 Length
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Bowser L.,
Tones T.,
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RESULT
Q9LDR9
                                                                                                                                                                                                                  Cheuk R., Shinn P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Thaveri A., Toriumi M., Vaysberg M., Yu G., Davis R., Federspiel N., Theologis A., Ecker J.;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core e
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
SEQUENCE FROM
                                                                                                           Cho H.,
                                          Submitted
                                                                                                                              STRAIN=CV.
                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (FEB-2000) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted
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01-DEC-2001
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01-OCT-2000
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                                                                      "Expansin AtEXP10 affects
                                                                                                                                                        SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                         Cosgrove D.J
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                                       (JAN-2000)
                                                                                                                                                                                               (JUL-2000)
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                                                                                                                              COLUMBIA;
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Last sequence update)
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edons; core eudicots; Rosidae;
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Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                       BLOSUM62
  October 11, 2002, 14:51:00; Search time 19.6871 Seconds (without alignments) 2003.488 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                              1 AGGGWVNAHATFYGGGDASG.....NNXANAGWSFGQTFTGAHVR 228
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1259
                                                                                                                                                                                                                                                                                                                                                                562222 seqs, 172994929 residues
                                                                                                                                                                                                                                                                                                                                                                                         Gapop 10.0 , Gapext 0.5
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sp_vertebrate:*
sp_unclassified:*
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sp_invertebrate:*
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pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

| Result<br>No. | Score  | Query | Length | DB | ID     | Description        |
|---------------|--------|-------|--------|----|--------|--------------------|
| 1             | 1246   | 99.0  | 237    | 10 | Q38863 | Q38863 arabidopsis |
| 2             | 1246   | 99.0  | 250    | 10 | Q9C554 | Q9c554 arabidopsis |
| ω             | 1139   | 90.5  | 249    | 10 | Q9LDR9 | Q9ldr9 arabidopsis |
| 4             | 1137   | 90.3  | 252    | 10 | Q9FUM2 | Q9fum2 prunus aviu |
| σı            | 1120   | 89.0  | 249    | 10 | Q93XP1 | Q93xp1 prunus cera |
| σ             | 1115   | 88.6  | 248    | 10 | 080622 | O80622 arabidopsis |
| 7             | 1106.5 | 87.9  | 249    | 10 | Q9M515 | Q9m5i5 triphysaria |
| œ             | 1092   | 86.7  | 249    | 10 | Q9ZP36 | Q9zp36 nicotiana t |
| 9             | 1090   | 86.6  | 247    | 10 | Q9M517 | Q9m5i7 triphysaria |
| 10            | 1051.5 | 83.5  | 242    | 10 | Q9LLB1 | Q9llb1 zinnia eleg |
| 11            | 1049   | 83.3  | 250    | 10 | Q9FVG9 | Q9fvg9 lycopersico |
| 12            | 1047   | 83.2  | 232    | 10 | P93493 | P93493 pinus taeda |
| 13            | 1047   | 83.2  | 253    | 10 | Q9SWY1 | Q9swy1 pinus taeda |
| 14            | 1046   | 83.1  | 245    | 10 | Q9LLB2 | Q9llb2 zinnia eleg |
| 15            | 1042   | 82.8  | 232    | 10 | P93492 | P93492 pinus taeda |
| 16            | 1037   | 82.4  | 253    | 10 | Q93XP2 | Q93xp2 prunus cera |

| C C C C C C C C C C C C C C C C C C C                                                                                                                                                                                                                                                                           | 117<br>118<br>119<br>119<br>120<br>121<br>121<br>122<br>123<br>124<br>125<br>126<br>127<br>128                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
|-----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1000<br>994<br>994<br>985<br>985<br>976.5<br>973.9<br>973.9<br>973.9<br>973.9<br>973.9<br>973.9                                                                                                                                                                                                                 | 1037<br>1037<br>1036<br>1034<br>1029<br>1028.5<br>1028.5<br>1026.5<br>1026.5<br>1026.5<br>1026.1026<br>1020<br>1020                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 79.4<br>79.1<br>79.0<br>78.9<br>78.5<br>77.8<br>77.8<br>77.3<br>77.3<br>74.3                                                                                                                                                                                                                                    | 82.4<br>82.4<br>82.3<br>82.1<br>82.1<br>81.7<br>81.7<br>81.5<br>81.5<br>81.5<br>81.5<br>81.5<br>81.5                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               |
| 2946<br>291<br>253<br>253<br>253<br>253<br>253<br>253<br>253<br>257<br>257                                                                                                                                                                                                                                      | 254<br>254<br>254<br>254<br>253<br>253<br>253<br>253<br>253<br>253<br>253<br>253<br>253<br>253                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     |
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| 09460<br>094601<br>094601<br>094807<br>094804<br>095800<br>020636<br>020636<br>020874<br>095801<br>048194<br>048194<br>048194<br>048194<br>048194<br>048194                                                                                                                                                     | 082093<br>093495<br>993495<br>09FUM3<br>09FZ35<br>09FZ35<br>09FZ35<br>09FZ35<br>09FZ35<br>09FZ35<br>09FZ35<br>081133<br>039FZ3<br>08125<br>08125<br>08125<br>08125<br>08125<br>08125<br>08125<br>08125<br>08125<br>08125<br>08125                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  |
| Q946JU OLYZG SALLY<br>Q9m4x8 OYYZG SALLY<br>Q946J1 OYYZA SALLY<br>Q94kt7 zea mays (m<br>Q9swd4 rumex palus<br>Q9fma0 arabidopsis<br>Q40636 oryza sativ<br>Q22874 arabidopsis<br>Q9fnt1 cicer ariet<br>Q9ayr1 eustoma gra<br>Q4818 arabidopsis<br>Q9sdz4 marsilea gu<br>Q9sqj6 lycopersico<br>Q9fy30 festuca pra | prunus cicer pinus prunus nicoti prunus nicoti prunus nicoti prunus nicoti prunus pinus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |

# ALIGNMENTS

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| 1 AGGGWVNAHATFYGGGDASGTMGGACGYGNLYSQGYGTNTAALSTALFNNGLSCGACFEI 60<br> | Query Match 99.0%; Score 1246; DB 10; Length 237;<br>Best Local Similarity 98.7%; Pred. No. 1.5e-105;<br>Matches 225; Conservative 1; Mismatches 2; Indels 0; Gaps | Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRELIMINARY; PRT; 237 AA. Q38863 PRT; 237 AA. Q38863 PRT; 237 AA. Q38863 PRT; 237 AA. Q38863 PRT; 237 AA. Q38863 PRT; PRT; 237 AA. Q38863 PRT; PRT; 237 AA. Q38863 PRT; Q37 AA. Q38863 PRT; 237 AA. Q38863 PRT; Q37 AA. Q38863 PRT; 237 AA. Q38868 PRT; 237 AA. Q38868 PRT; 237 AA. Q38868 PRT; 237 AA. Q3886 |  |

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